

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 8, 2005, 02:19:48 ; Search time 165 Seconds
(without alignments)
673.188 Million cell updates/sec

Title: US-10-657-852B-15

Perfect score: 1385

Sequence: 1 MPEYMAKCCMLLVFLGFIQ.....NTVSGSNHIVSGSNKVVTDG 267

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1854112 seqs, 416015017 residues

Total number of hits satisfying chosen parameters: 1854112

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1385	100.0	267	18	US-10-657-852-16
2	1290	93.1	269	18	US-10-657-852-17
3	992.5	71.7	262	18	US-10-657-852-24
4	980.5	70.8	254	18	US-10-657-852-23
5	973.5	70.3	256	18	US-10-657-852-25
6	910.5	65.7	277	18	US-10-657-852-20
7	908.5	65.6	277	18	US-10-657-852-19
8	904.5	65.3	281	18	US-10-657-852-26
9	901.5	65.1	281	18	US-10-657-852-18
10	901.5	65.1	285	18	US-10-657-852-22
11	884	63.8	280	18	US-10-657-852-21

12	668	48.2	243	18	US-10-657-852-15	Sequence 15, Appl
13	655	47.3	243	18	US-10-657-852-14	Sequence 14, Appl
14	262	18.9	1010	16	US-10-437-963-180288	Sequence 180288
15	206.5	14.9	1039	16	US-10-437-963-166082	Sequence 166082
16	204	14.7	1021	15	US-10-443-101-2	Sequence 2, Appli
17	204	14.7	1021	17	US-10-733-923-1223	Sequence 1223, Ap
18	198	14.3	264	16	US-10-437-963-148813	Sequence 148813
19	197	14.2	961	16	US-10-437-963-172660	Sequence 172660
20	194	14.0	917	16	US-10-437-963-115627	Sequence 115627
21	194	14.0	1164	16	US-10-437-963-192784	Sequence 192784
22	192.5	13.9	938	16	US-10-437-963-189754	Sequence 189754
23	192	13.9	1060	16	US-10-437-963-153194	Sequence 153194
24	190	13.7	1044	16	US-10-437-963-162505	Sequence 162505
25	188.5	13.6	1011	16	US-10-437-963-172329	Sequence 172329
26	188.5	13.6	1078	16	US-10-437-963-123119	Sequence 123119
27	186	13.4	278	15	US-10-424-599-267766	Sequence 267766
28	186	13.4	676	16	US-10-437-963-153306	Sequence 153306
29	185	13.4	1012	16	US-10-437-963-192786	Sequence 192786
30	183.5	13.2	380	16	US-10-437-963-136619	Sequence 136619
31	183.5	13.2	1133	16	US-10-437-963-150876	Sequence 150876
32	183.5	13.2	1140	16	US-10-437-963-119802	Sequence 119802
33	182	13.1	941	10	US-09-952-267-9	Sequence 9, Appli
34	182	13.1	941	18	US-10-872-768-9	Sequence 9, Appli
35	182	13.1	941	18	US-10-872-769-9	Sequence 9, Appli
36	182	13.1	1231	16	US-10-437-963-102913	Sequence 102913
37	181	13.1	653	15	US-10-389-566-1625	Sequence 1625, Ap
38	181	13.1	1065	16	US-10-437-963-109994	Sequence 109994
39	181	13.1	1469	16	US-10-437-963-196963	Sequence 196963
40	180.5	13.0	675	16	US-10-437-963-174437	Sequence 174437
41	180	13.0	1036	16	US-10-437-963-149679	Sequence 149679
42	180	13.0	1080	16	US-10-437-963-110291	Sequence 110291
43	179	12.9	516	15	US-10-424-599-201138	Sequence 201138
44	178	12.9	143	16	US-10-425-115-295330	Sequence 295330
45	178	12.9	153	15	US-10-425-114-63986	Sequence 63986, A

ALIGNMENTS

RESULT 1
US-10-657-852-16
; Sequence 16, Application US/10657852
; Publication No. US20040146884A1
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jercoen
; APPLICANT: Shenk, Michael Andrew
; APPLICANT: Hall, Claire
; APPLICANT: Fish, Steven A
; TITLE OF INVENTION: Antifreeze proteins isolated from forage
; TITLE OF INVENTION: Grasses and methods for their use.
; FILE REFERENCE: 11000.1070U
; CURRENT APPLICATION NUMBER: US/10/657,852
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/409,557
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Festuca arundinacea
US-10-657-852-16

Query Match	100.0%	Score 1385;	DB 18;	Length 267;
Best Local Similarity	100.0%;	Pred. No. 1.9e-111;		
Matches 267;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MPEYMAKCCMLLVFLGFIQVAGATSWSCHDDHLALGIAENLSGKGVRLRAAWSGAS	60	
Db	1	MPEYMAKCCMLLVFLGFIQVAGATSWSCHDDHLALGIAENLSGKGVRLRAAWSGAS	60	
QY	61	CCSWEVGVCETASGRVVALRLPKRGLGGIIPSSIGBELDHLRYLDLSGNSLVGVPKSLQI	120	

```

Db 61 CCSWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRLYLDLSGNSLVGEVPKSLQI 120
QY 121 RLKSLTTDSQSLGMSINMLLVHSRRRLTDEEPTISGTNNVSGSGNNVSGNDNTVVS 180
Db 121 RLKSLTTDSQSLGMSINMLLVHSRRRLTDEEPTISGTNNVSGSGNNVSGNDNTVVS 180
QY 181 GNNNHVSGSNNVTVTGSDNTVVGSHVSGTKHIVTDNNNNVSGNDNNVSGSFHTVSGEH 240
Db 181 GNNNHVSGSNNVTVTGSDNTVVGSHVSGTKHIVTDNNNNVSGNDNNVSGSFHTVSGEH 240
QY 241 NTVSGSNNVTVSGSNHIVSGSNKVVTGD 267
Db 241 NTVSGSNNVTVSGSNHIVSGSNKVVTGD 267

```

RESULT 2

```

US-10-657-852-17
; Sequence 17, Application US/10657852
; Publication No. US20040146884A1
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jeroen
; APPLICANT: Shenk, Michael Andrew
; APPLICANT: Hall, Claire
; TITLE OF INVENTION: Antifreeze proteins isolated from forage
; TITLE OF INVENTION: Grasses and methods for their use.
; FILE REFERENCE: 11000.10700
; CURRENT APPLICATION NUMBER: US/10/657,852
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/409,557
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Festuca arundinacea
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(269)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-657-852-17

```

```

Query Match 93.1%; Score 1290; DB 18; Length 269;
Best Local Similarity 93.3%; Pred. No. 3.1e-103;
Matches 251; Conservative 6; Mismatches 10; Indels 2; Gaps 2;

QY 1 MPEYMAKCCMLLVFLGFI-LQVAGATWSCHHDDLHALRGLAENLSGKGAVALRLAAWSGA 59
Db 1 MPEYMAKCCMLLVLLAFILLQVAGATWSCHHDDLALRGFAENLSGKGAVALRLAAWSGA 60
QY 60 CCSWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRLYLDLSGNSLVGEVPKSLQ 119
Db 61 CCSWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRLYLDLSGNSLVGEVPKSLQ 120
QY 120 IRLKSLTTDSQSLGMSINMLLVHS--RRTLDEEPTISGTNNVSGSGNNVSGNDNTV 178
Db 121 IRLKSLTTDSQSLGMSINMLLVHSNRRLTDEEPTISGTNNVSGSGNNVSGNDNTV 180
QY 179 VSGNNNHVSGSNNVTVTGSDNTVVGSHVSGTKHIVTDNNNNVSGNDNNVSGSFHTVSG 238
Db 181 ISGNNNHVSGSNNVTVTGSDNTLVGSHVSGTKHIVTDNNNNVSGNDNNVSGSFHTVSG 240
QY 239 EHNVTSGSNNVTVSGSNHIVSGSNKVVTGD 267
Db 241 EHNVTSGSNNVTVSGSNHIVSGSNKVVTGD 269

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RESULT 3

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US-10-657-852-24
; Sequence 24, Application US/10657852
; Publication No. US20040146884A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Demmer, Jeroen
; APPLICANT: Shenk, Michael Andrew
; APPLICANT: Hall, Claire
; APPLICANT: Fish, Steven A
; TITLE OF INVENTION: Antifreeze proteins isolated from forage
; TITLE OF INVENTION: Grasses and methods for their use.
; FILE REFERENCE: 11000.10700
; CURRENT APPLICATION NUMBER: US/10/657,852
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/409,557
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Festuca arundinacea
US-10-657-852-24

Query Match 71.7%; Score 992.5; DB 18; Length 262;
Best Local Similarity 75.0%; Pred. No. 1.6e-77;
Matches 198; Conservative 22; Mismatches 39; Indels 5; Gaps 3;

QY 5 MAKCCMLLVFLGFILOVAG-ATWSCHHDDLHALRGLAENLSGKGAVALRLAAWSGASCCS 63
Db 1 MAKCLMLLLSFAFLLSAAGTATATPCHRDDLALRGFAENLGGGALSRLAAWSGASCCD 60
QY 64 WEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRLYLDLSGNSLVGEVPKSLQIRLK 123
Db 61 WEGVGCDSAGREVTAALWLPRLSGLTGPIPSWICQLHRLYLDLSGNALVGEVPKNLQVQLK 120
QY 124 SLTDSQSLGMSINMLLVH--SSRRTLDEEPTISGTNNVSGSGNNVSGNDNTVVS 182
Db 121 GLTAAGRS---GFTNNPLHVNRRLSDEQPNITSGSNNTVRSKKNVVGAGNDNTVISGD 177
QY 183 NNHVSGSNNVTVTGSDNTVVGSHVSGTKHIVTDNNNNVSGNDNNVSGSFHTVSGEHNT 242
Db 178 NNSVSGSNNVTVTGSDNTVVGSHVSGTNNHIVTDNNNNVSGNDNNVSGSFHTVSGEHNT 237
QY 243 VSGSNNTVSGSNHIVSGSNKVVTVD 266
Db 238 VSGSNNTVSGSNHIVSGSNKVVTVD 261

```

RESULT 4

```

US-10-657-852-23
; Sequence 23, Application US/10657852
; Publication No. US20040146884A1
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jeroen
; APPLICANT: Shenk, Michael Andrew
; APPLICANT: Hall, Claire
; APPLICANT: Fish, Steven A
; TITLE OF INVENTION: Antifreeze proteins isolated from forage
; TITLE OF INVENTION: Grasses and methods for their use.
; FILE REFERENCE: 11000.10700
; CURRENT APPLICATION NUMBER: US/10/657,852
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/409,557
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Festuca arundinacea
US-10-657-852-23

```

```

Query Match 70.8%; Score 980.5; DB 18; Length 254;
Best Local Similarity 73.5%; Pred. No. 1.7e-76;
Matches 194; Conservative 24; Mismatches 33; Indels 13; Gaps 3;

QY 5 MAKCCMLLVFLGFILOVAG-ATWSCHHDDLHALRGLAENLSGKGAVALRLAAWSGASCCS 63

```

```
Db 1 MAKCLMLLSFAFLLSVAGTATATPCRRDRLRALRGAENLGGGGAISLRAAWSGASCCD 60
Qy 64 WEGVGCTASGRVVALRPKRGLGGIIPSSIGELDLHLRYLDLSGSLVGEVPKSLQIRLK 123
Db 61 WEGVGCDGASGRVTALWPRSGLTGTPSWICQLHLRYLDLSGNALVGEVPKNLQVLK 120
Qy 124 SLTTDSQSGLMGSIINMLLHV--SSRRTLDEEPNTISGTNNVSGSNVSGNDNTVVSQN 182
Db 121 GIT-----NMPLHVMNRRLSDEQNTISGNNNTVSGSNKVLAGNDNTVISGD 169
Qy 183 NNHVSNNNTVVTGSDNTVVSNNHVSCTKHIVTDNNNVSGNDNNVSGSFHTVSGEHT 242
Db 170 NNSVSGSNNTVVSNDNTVVSNNHVSCTKHIVTDNNNVSGNDNNVSGSFHTVSGGHT 229
Qy 243 VSGSNNTVSGSNHVSNNKVVTD 266
Db 230 VSGSNNTVSGSNHVSNNKVVTD 253
```

```
RESULT 5
US-10-657-852-25
Query Match 70.3%; Score 973.5; DB 18; Length 256;
Best Local Similarity 72.6%; Pred. No. 6.8e-76;
Matches 193; Conservative 24; Mismatches 34; Indels 15; Gaps 3;
; Publication No. US20040146884A1
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jeroen
; APPLICANT: Shenk, Michael Andrew
; APPLICANT: Hall, Claire
; APPLICANT: Fish, Steven A
; TITLE OF INVENTION: Antifreeze proteins isolated from forage
; FILE REFERENCE: 11000.10700
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/409,557
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Festuca arundinacea
US-10-657-852-25
```

```
Query Match 70.3%; Score 973.5; DB 18; Length 256;
Best Local Similarity 72.6%; Pred. No. 6.8e-76;
Matches 193; Conservative 24; Mismatches 34; Indels 15; Gaps 3;
; Publication No. US20040146884A1
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jeroen
; APPLICANT: Shenk, Michael Andrew
; APPLICANT: Hall, Claire
; APPLICANT: Fish, Steven A
; TITLE OF INVENTION: Antifreeze proteins isolated from forage
; FILE REFERENCE: 11000.10700
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/409,557
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Festuca arundinacea
US-10-657-852-25
```

```
RESULT 6
US-10-657-852-20
Query Match 65.6%; Score 908.5; DB 18; Length 277;
Best Local Similarity 67.9%; Pred. No. 3.1e-70;
Matches 188; Conservative 19; Mismatches 51; Indels 19; Gaps 4;
; Publication No. US20040146884A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jeroen
; APPLICANT: Shenk, Michael Andrew
; APPLICANT: Hall, Claire
; APPLICANT: Fish, Steven A
; TITLE OF INVENTION: Antifreeze proteins isolated from forage
; FILE REFERENCE: 11000.10700
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/409,557
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Festuca arundinacea
US-10-657-852-20
```

```
Query Match 65.7%; Score 910.5; DB 18; Length 277;
Best Local Similarity 67.5%; Pred. No. 2.1e-70;
Matches 187; Conservative 20; Mismatches 51; Indels 19; Gaps 4;
; Publication No. US20040146884A1
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jeroen
; APPLICANT: Shenk, Michael Andrew
; APPLICANT: Hall, Claire
; APPLICANT: Fish, Steven A
; TITLE OF INVENTION: Antifreeze proteins isolated from forage
; FILE REFERENCE: 11000.10700
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/409,557
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Festuca arundinacea
US-10-657-852-20
```

```
RESULT 7
US-10-657-852-19
Query Match 65.7%; Score 910.5; DB 18; Length 277;
Best Local Similarity 67.5%; Pred. No. 2.1e-70;
Matches 187; Conservative 20; Mismatches 51; Indels 19; Gaps 4;
; Publication No. US20040146884A1
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jeroen
; APPLICANT: Shenk, Michael Andrew
; APPLICANT: Hall, Claire
; APPLICANT: Fish, Steven A
; TITLE OF INVENTION: Antifreeze proteins isolated from forage
; FILE REFERENCE: 11000.10700
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/409,557
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Festuca arundinacea
US-10-657-852-19
```

```
Query Match 65.6%; Score 908.5; DB 18; Length 277;
Best Local Similarity 67.9%; Pred. No. 3.1e-70;
Matches 188; Conservative 19; Mismatches 51; Indels 19; Gaps 4;
; Publication No. US20040146884A1
```

```
QY 5 MAKCCMLLVFLGFILOVAGATWSCHHDDLHALRGLAENLSGKGAVALRAAASGASCCSW 64
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 1 MAKCCMLLVFLGFILOVAGATWSCHHDDLHALRGLAENLSGKGAVALRAAASGASCCSW 57
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 65 EGVGCETASGRVVALRLP-----KRLGGIIPSSIGELDLHLYLDLSGNS 109
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 58 EGVGCDGTSGRVTALRLPISLDCGKLSLNLANERLVGTIPSWIGELDHCHLYLSDNS 117
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 110 LVGEVPSLQIRLKSITTDOSQSLGMSINMLLHV--SSRRTLDEPNTTSGTNNVSGSN 168
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 118 LVGKPNLSLQIRLKSITTDOSQSLGMSINMLLHV--SSRRTLDEPNTTSGTNNVSGSN 177
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 169 NVSGNNDNTVSGNNHVSNNVTGSDNTVSGSNHVSNNHVSNNHVSNNHVSNNHVSNN 228
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 178 NAVSGNDNTVICNNNTVSGNNHVSNNVTGSDNTVSGSNHVSNNHVSNNHVSNNHVSNN 237
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 229 VSGSGFHTVSGHNTVSGNNHVSNNHVSNNHVSNNHVSNNHVSNNHVSNNHVSNN 265
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 238 VSGSGHNTVSGHNTVSGNNHVSNNHVSNNHVSNNHVSNNHVSNNHVSNNHVSNN 274
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
```

RESULT 8

```
US-10-657-852-26
; Sequence 26, Application US/10657852
; Publication No. US20040146884A1
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jeroen
; APPLICANT: Shenk, Michael Andrew
; APPLICANT: Hall, Claire
; APPLICANT: Fish, Steven A
; TITLE OF INVENTION: Antifreeze proteins isolated from forage
; FILE REFERENCE: 11000.10700
; CURRENT APPLICATION NUMBER: US/10/657,852
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/409,557
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-657-852-26
```

```
Query Match 65.3%; Score 904.5; DB 18; Length 281;
Best Local Similarity 66.5%; Pred. No. 7.1e-70; Indels 23; Gaps 5;
Matches 187; Conservative 20; Mismatches 51;

QY 5 MAKCCMLLVFLGFILOVAGATWSCHHDDLHALRGLAENLSGKGAVALRAAASGASCCSW 64
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 1 MAKCCMLLVFLGFILOVAGATWSCHHDDLHALRGLAENLSGKGAVALRAAASGASCCSW 57
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 65 EGVGCETASGRVVALRLP-----KRLGGIIPSSIGELDLHLYLDLSGNS 109
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 58 EGVGCDGTSGRVTALRLPISLDCGKLSLNLANERLVGTIPSWIGELDHCHLYLSDNS 117
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 110 LVGEVPSLQIRLKSITTDOSQSLGMSINMLLHV--SSRRTLDEPNTTSGTNNVSG 164
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 118 LVGKPNLSLQIRLKSITTDOSQSLGMSINMLLHV--SSRRTLDEPNTTSGTNNVSG 177
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 165 SGNNVSGNNDNTVSGNNHVSNNVTGSDNTVSGSNHVSNNHVSNNHVSNNHVSNNHVSNN 224
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 178 SGNDNAVSGNDNTVICNNNTVSGNNHVSNNVTGSDNTVSGSNHVSNNHVSNNHVSNNHVSNN 237
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 225 NDNNVSGSFHTVSGHNTVSGNNHVSNNHVSNNHVSNNHVSNNHVSNNHVSNNHVSNN 265
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 238 NDNNVSGSFHTVSGHNTVSGNNHVSNNHVSNNHVSNNHVSNNHVSNNHVSNNHVSNN 278
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
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RESULT 9

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US-10-657-852-18
; Sequence 18, Application US/10657852
```

```
; Publication No. US20040146884A1
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jeroen
; APPLICANT: Shenk, Michael Andrew
; APPLICANT: Hall, Claire
; APPLICANT: Fish, Steven A
; TITLE OF INVENTION: Antifreeze proteins isolated from forage
; FILE REFERENCE: 11000.10700
; CURRENT APPLICATION NUMBER: US/10/657,852
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/409,557
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Festuca arundinacea
US-10-657-852-18
```

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Query Match 65.1%; Score 901.5; DB 18; Length 281;
Best Local Similarity 66.2%; Pred. No. 1.3e-69;
Matches 186; Conservative 21; Mismatches 51; Indels 23; Gaps 5;

QY 5 MAKCCMLLVFLGFILOVAGATWSCHHDDLHALRGLAENLSGKGAVALRAAASGASCCSW 64
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 1 MAKCCMLLVFLGFILOVAGATWSCHHDDLHALRGLAENLSGKGAVALRAAASGASCCSW 57
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 65 EGVGCETASGRVVALRLP-----KRLGGIIPSSIGELDLHLYLDLSGNS 109
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 58 EGVGCDGTSGRVTALRLPISLDCGKLSLNLANERLVGTIPSWIGELDHCHLYLSDNS 117
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 110 LVGEVPSLQIRLKSITTDOSQSLGMSINMLLHV--SSRRTLDEPNTTSGTNNVSG 164
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 118 LVGKPNLSLQIRLKSITTDOSQSLGMSINMLLHV--SSRRTLDEPNTTSGTNNVSG 177
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 165 SGNNVSGNNDNTVSGNNHVSNNVTGSDNTVSGSNHVSNNHVSNNHVSNNHVSNNHVSNN 224
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 178 SGNDNAVSGNDNTVICNNNTVSGNNHVSNNVTGSDNTVSGSNHVSNNHVSNNHVSNNHVSNN 237
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 225 NDNNVSGSFHTVSGHNTVSGNNHVSNNHVSNNHVSNNHVSNNHVSNNHVSNNHVSNN 265
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 238 NDNNVSGSFHTVSGHNTVSGNNHVSNNHVSNNHVSNNHVSNNHVSNNHVSNNHVSNN 278
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
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RESULT 10

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US-10-657-852-22
; Sequence 22, Application US/10657852
; Publication No. US20040146884A1
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jeroen
; APPLICANT: Shenk, Michael Andrew
; APPLICANT: Hall, Claire
; APPLICANT: Fish, Steven A
; TITLE OF INVENTION: Antifreeze proteins isolated from forage
; FILE REFERENCE: 11000.10700
; CURRENT APPLICATION NUMBER: US/10/657,852
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/409,557
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Festuca arundinacea
US-10-657-852-22
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Query Match 65.1%; Score 901.5; DB 18; Length 285;
Best Local Similarity 65.5%; Pred. No. 1.3e-69;
Matches 186; Conservative 17; Mismatches 54; Indels 27; Gaps 3;
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	Matches	148;	Conservative	18;	Mismatches	55;	Indels	64;	Gaps	57
Qy	5	MAKCCMLLVFLGFILOVAGATSWCHDDDLHALRGLAENLSGKGAVRLRAAWSGASCSCW	64							
Db	1	MAKCWQLLLFLALLLPAASAA--SCHPPDYLRLDFAGNLRG-GGVLLRALPAGSACGW	57							
Qy	65	EGVGCEATSGRVVALRPLKRG LGGIIPSSIGELDHRLYLDLSGNSLVCEVPKSLQIRUKS	124							
Db	58	EGVGCDGASGCV-----KSQILLKG	78							
Qy	125	LTTDSQSLGMSINMLLHVS-SRRTLEEPNTISGTNNVSGSGSNVVSGNDNTTVVSGNN	183							
Db	79	LTAAGRSLGKAFTMPLHVKPSQGLTDEHDHTITGINNVTRSGSNVVVSGNDNTVISGN	138							
Qy	184	NHYVSGSNNTVVTGSDNTVGSNGHHVSVGTHKLTVDNNVVSGNDNNVSGSFHTVSGEHTV	243							
Db	139	NVTVSGSHNTVVFSGDNFISGSHVYVSGNHVHTTDNKNAVSGDHTVSGSQNTVSGNHQIV	198							
Qy	244	SGS-----NNTVSGSNHIVSGSKNVYTGD	267							
Db	199	SGSHSTVSGNHNTVSGRNNSVYGNNNIYVSGSNHHVYGGNNKVVTGG	243							

```

RESULT 14
US-10-437-963-180288
; Sequence 180288, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 180288
; LENGTH: 1010
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_7766C.1.pep
US-10-437-963-180288

```

RESULT 15
US-10-437-963-166082
; Sequence 166082, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.

[illegible]

Db 119 LQELNLASNGLS-GTIPYSISNMTGLTDLKLSHNQLSGQIQDIFGQLSSLSLTLDLSFNTL 177
Qy 157 SGT-----NNSVSGSGNNVSGNDNTVVSGNNHVS----- 188
Db 178 TQNLPOSFSSLSLSVLYLQNNQL-AGSVNVLNPLTDLTNIENNRFSGVPNWRSNQN 236
Qy 189 ----SNNVTVG-----SDNTVSGNHVV---SGPKHIVTDNNVVSNDNN 228
Db 237 FKYSNGSFATGAPPPPPPTPPPPNNRPPKSSNVVPSGGSK-----GGNSNK 286
Qy 229 VSGSFHTVSG 238
Db 287 KSLSGGAIVG 296
RESULT 12
US-10-101-464A-80
; Sequence 80, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Pinus radiata
US-10-101-464A-80
Query Match 12.3%; Score 170.5; DB 4; Length 707;
Best Local Similarity 26.1%; Pred. No. 8.9e-08;
Matches 81; Conservative 39; Mismatches 89; Indels 101; Gaps 16;
Qy 9 CMLLVFLGFIQVA---GATSWSCHDDLHLRGLAENLSGKGAVRLRAWS--GASCC- 62
Db 8 CURLIAILTASTAISGHGTTD----PDVSAKGIYSSLSNPQOL---SGWSANGDPCG 60
Qy 63 -SWEVGVCETASGRVVVALRPKRGLGIIIPSSIGELDLRLYLDLSGNSLVGEVPKSLQIR 121
Db 61 QSWKGVCSGSS--VTILKLSGLGSLYYQLSDLSSTLTLDLSNNIQGNIPALPK 118
Qy 122 LKSLTTDSQSLMGSI-----NM-----LH------VSSRRITLDEPNTI 156
Db 119 LQELNLASNGLS-GTIPYSISNMTGLTDLKLSHNQLSGQIQDIFGQLSSLSLTLDLSFNTL 177
Qy 157 SGT-----NNSVSGSGNNVSGNDNTVVSGNNHVS----- 188
Db 178 TQNLPOSFSSLSLSVLYLQNNQL-AGSVNVLNPLTDLTNIENNRFSGVPNWRSNQN 236
Qy 189 ----SNNVTVG-----SDNTVSGNHVV---SGPKHIVTDNNVVSNDNN 228
Db 237 FKYSNGSFATGAPPPPPPTPPPPNNRPPKSSNVVPSGGSK-----GGNSNK 286
Qy 229 VSGSFHTVSG 238
Db 287 KSLSGGAIVG 296

RESULT 13
US-09-336-447A-7
; Sequence 7, Application US/09336447A
; Patent No. 6310190
; GENERAL INFORMATION:
; APPLICANT: HANSEN, ERIC J.
; APPLICANT: AEBI, CHRISTOPH
; APPLICANT: COPE, LESLIE D.
; APPLICANT: MACIVER, ISOBEL
; APPLICANT: FISKE, MICHAEL J.
; APPLICANT: FREDENBURG, ROSS A.
; TITLE OF INVENTION: USP1 AND USP2 ANTIGENS OF MORAXELLA CATARRHALIS
; FILE REFERENCE: AMCY:024
; CURRENT APPLICATION NUMBER: US/09/336,447A
; CURRENT FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 624
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-336-447A-7
Query Match 12.3%; Score 170; DB 3; Length 624;
Best Local Similarity 30.6%; Pred. No. 8.3e-08;
Matches 38; Conservative 24; Mismatches 50; Indels 12; Gaps 2;
Qy 154 NTISGTNNSVSGSGNNVSGNDNTVVSGNNHVSNNNTVVTGSDNTVVSGNNHVSGETKH 213
Db 104 NQAKGEHSTIAGGESNQATGRNSTVAGGSNNQAVGTNSTVAGGSNNQAKGANSFAAGVGN 163
Qy 214 IVTDNNNVSGNDNVSGSFHTVSGEHTVS-----GNNNTVSGSNHIVSG---SN 261
Db 164 QANTNAVALGKNNTINGNNSAAIGSENTVNENQKNVFILGNTTNAQSGVLLGHETSG 223
Qy 262 KVVVT 265
Db 224 KEAT 227
RESULT 14
US-09-952-267B-7
; Sequence 7, Application US/09952267B
; Patent No. 6753417
; GENERAL INFORMATION:
; APPLICANT: HANSEN, ERIC J.
; APPLICANT: AEBI, CHRISTOPH
; APPLICANT: COPE, LESLIE D.
; APPLICANT: MACIVER, ISOBEL
; APPLICANT: FISKE, MICHAEL J.
; APPLICANT: FREDENBURG, ROSS A.
; TITLE OF INVENTION: USP1 AND USP2 ANTIGENS OF MORAXELLA CATARRHALIS
; FILE REFERENCE: AMCY:024
; CURRENT APPLICATION NUMBER: US/09/952,267B
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US/09/336,447
; PRIOR FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 624
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-952-267B-7
Query Match 12.3%; Score 170; DB 4; Length 624;
Best Local Similarity 30.6%; Pred. No. 8.3e-08;
Matches 38; Conservative 24; Mismatches 50; Indels 12; Gaps 2;
Qy 154 NTISGTNNSVSGSGNNVSGNDNTVVSGNNHVSNNNTVVTGSDNTVVSGNNHVSGETKH 213
Db 104 NQAKGEHSTIAGGESNQATGRNSTVAGGSNNQAVGTNSTVAGGSNNQAKGANSFAAGVGN 163


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Db 253 SRLVLETLFFDNDISGISPASINCTSLQVLDISMSLSP-----IPSEFRL 303
QY 222 VS-----GNDNVSGSFHTVSGEHTVS---GNNVTGSGNHVSGSNKVV 265
Db 304 VSLESYLFDNDSISGIPFLVNCSTLSALGASGNKLSGSPVSMGLMKNIS 355

RESULT 9
US-10-101-464A-764
; Sequence 764, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10101464A
; PRIOR FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 764
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Pinus radiata
US-10-101-464A-764

Query Match 12.4%; Score 171.5; DB 4; Length 323;
Best Local Similarity 25.5%; Pred. No. 2.4e-08;
Matches 82; Conservative 52; Mismatches 112; Indels 75; Gaps 14;

QY 10 MLLVFLGFTL-----OVAGATWSCHHD--DLHALRGLAE--NL 44
Db 6 LLLVMGVAMPHTSQHTGFTSVORPPFNGRSMGKPSIAGYHEKEDVALLSFRKGITL 65
QY 45 SGKGAVRLRAAWSGSCSWEGVCGTASGRVVALRPLKRGGLGIIPISSIGELDLHLRYLD 104
Db 66 DPYGLSNNTANNHNVCLWNGISCPNTRNVEISRYGRLNGTLSPYIGNLSLRLHLD 125
QY 105 LSGNSLVGVPKSL-----QIRLKSLLTDSQS-----LGMGSINMLLVSSRRLDEPN 154
Db 126 LSSNALSGRIPAEFGOLKALRIIDLNNALTGSIPTCIGNGLNGTL-----DLDSLWN 179
QY 155 TISG-----TNNSVSGNNVSGNDNTVSGNN--NHVSGNNVTVV- 194
Db 180 AFSGRIPKELFNTRLQRIOLDSHNSL-TGSIPTSGNALLQTLNFGNYLSGSIPTSLA 238
QY 195 --TGSDNTVGSNNHVSQTKHIVTDNNNVVS-----GNDNNVSGSFHTVSGEHT--VS 244
Db 239 NCTSLTDLVSSNN-LSGP--IPSEFGLVSLKFLFLDDNDSIGSIPSTSLVNCTSLFALK 295
QY 245 GSNNTVSGSNHIVSGSNKVV 265
Db 296 GSGNKLSGPPIPSVMGLMKSI 316

RESULT 10
US-10-101-464A-902
; Sequence 902, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas

```

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; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10101464A
; PRIOR FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 902
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Pinus radiata
US-10-101-464A-902

Query Match 12.3%; Score 170.5; DB 4; Length 386;
Best Local Similarity 32.3%; Pred. No. 3.8e-08;
Matches 52; Conservative 25; Mismatches 61; Indels 23; Gaps 7;

QY 29 CHHDLHALRGLAENLSGKAVRLRAAWS-GASCCSWEGVCGTASGR---VVALRLPKR 84
Db 38 CNQSDVQALISFKQTVSSSPLN---WEVNRSCCTWEGVTGGLLSLQOFSVTKURLPKR 93
QY 85 GLGGIIPSSIGELDLHLRYLDLSGNSLVGVPKSLQIRLKSLLTDSQSLSGMSINMLLHV- 143
Db 94 RLRTGLSDSLGELAHRLREINVSFNLLTGEVPCRLFL-LQHL--EVLDSLNNLSVIAPVA 150
QY 144 ---SSRRTLDEEPNTISGTNNVSGS-----SNNVVS 173
Db 151 OGLNSIRTFNITSNSFRGNVPOLGSAVNLTSFNVSNNSTFG 191

RESULT 11
US-09-228-986-80
; Sequence 80, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-228-986-80

Query Match 12.3%; Score 170.5; DB 3; Length 707;
Best Local Similarity 26.1%; Pred. No. 8.9e-08;
Matches 81; Conservative 39; Mismatches 89; Indels 101; Gaps 16;

QY 9 CMLLVFLGFILOVA---GATWSCHHDLHALRGLAENLSGKAVRLRAAWS--GASCC- 62
Db 8 CLRLIAILTASIAISHGTTD---PDDVSALKGIYSSLNSPQL---SGWSANGGDPG 60
QY 63 -SWEGVCGTASGRVVALRPLKRGGLIIPSSIGELDLHLRYLDLSGNSLVGVPKSLQIR 121
Db 61 QSWKGVCSGSS--VTLIKLSGLGLSGSLYYQISLSSLTLLDLSNNNQINIPALPK 118
QY 122 LKSLTTDSQSLGWSI-----NN-----LH-----VSSRRTLDEEPNTI 156

```



```
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US/09/336,447
; PRIOR FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 941
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-952-267B-9
```

```
Query Match      13.1%; Score 182; DB 4; Length 941;
Best Local Similarity 34.2%; Pred. No. 1e-08;
Matches 39; Conservative 19; Mismatches 50; Indels 6; Gaps 1;

QY 154 NTISGTNNVSGSNVYVSGNDNTVVGNNHVSNNNTVVTGSDNTVVGSNHVSNGTKH 213
Db 123 NEAMGEYSTVAGGANNQAGNSTYVGGNGNKAIGNNSTVVGSNQAKGEHSTIAGGK- 181

QY 214 IVTDNNVSGNDNNVSGSFHTVSGEHNNTVSGNNHVSNNHVSNNHVSNNKVVTDG 267
Db 182 -----NQATGGSFAGGVENKADANNAVALGNKNTIEGTNSVAIGSNNTVKTG 230
```

RESULT 3

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US-09-336-447A-5
; Sequence 5, Application US/09336447A
; Patent No. 6310190
; GENERAL INFORMATION:
; APPLICANT: HANSEN, ERIC J.
; APPLICANT: ABEI, CHRISTOPH
; APPLICANT: COPE, LESLIE D.
; APPLICANT: MACIVER, ISOBEL
; APPLICANT: FISKE, MICHAEL J.
; APPLICANT: FREDENBURG, ROSS A.
; TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
; FILE REFERENCE: AMCY:024
; CURRENT APPLICATION NUMBER: US/09/336,447A
; CURRENT FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 892
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-336-447A-5
```

```
Query Match      12.8%; Score 177; DB 3; Length 892;
Best Local Similarity 31.8%; Pred. No. 2.9e-08;
Matches 35; Conservative 20; Mismatches 49; Indels 6; Gaps 1;

QY 158 GTNNVSGSNVYVSGNDNTVVGNNHVSNNNTVVTGSDNTVVGSNHVSNGTKHIVTD 217
Db 143 GDSSTIGGGYNNQATGEKSTVAGGRNNQATGNNSTVAGGSYNQATGNNSTVAGGSH- 198

QY 218 NNNVSGNDNNVSGSFHTVSGEHNNTVSGNNHVSNNHVSNNHVSNNKVVTDG 267
Db 199 --NQATGGSFAGGVENKADANNAVALGNKNTIDGNSVAIGSNNTIDSG 246
```

RESULT 4

```
US-09-952-267B-5
; Sequence 5, Application US/09952267B
; Patent No. 6753417
; GENERAL INFORMATION:
; APPLICANT: HANSEN, ERIC J.
; APPLICANT: ABEI, CHRISTOPH
; APPLICANT: COPE, LESLIE D.
; APPLICANT: MACIVER, ISOBEL
; APPLICANT: FISKE, MICHAEL J.
; APPLICANT: FREDENBURG, ROSS A.
; TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
; FILE REFERENCE: AMCY:024
```

```
; CURRENT APPLICATION NUMBER: US/09/952,267B
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US/09/336,447
; PRIOR FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 892
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-952-267B-5
```

```
Query Match      12.8%; Score 177; DB 4; Length 892;
Best Local Similarity 31.8%; Pred. No. 2.9e-08;
Matches 35; Conservative 20; Mismatches 49; Indels 6; Gaps 1;

QY 158 GTNNVSGSNVYVSGNDNTVVGNNHVSNNNTVVTGSDNTVVGSNHVSNGTKHIVTD 217
Db 143 GDSSTIGGGYNNQATGEKSTVAGGRNNQATGNNSTVAGGSYNQATGNNSTVAGGSH- 198

QY 218 NNNVSGNDNNVSGSFHTVSGEHNNTVSGNNHVSNNHVSNNHVSNNKVVTDG 267
Db 199 --NQATGGSFAGGVENKADANNAVALGNKNTIDGNSVAIGSNNTIDSG 246
```

RESULT 5

```
US-10-101-464A-890
; Sequence 890, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 890
; LENGTH: 804
; TYPE: PRT
; ORGANISM: Pinus radiata
US-10-101-464A-890
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Query Match      12.7%; Score 176.5; DB 4; Length 804;
Best Local Similarity 23.4%; Pred. No. 2.8e-08;
Matches 77; Conservative 54; Mismatches 105; Indels 93; Gaps 13;

QY 10 MLLVFLGFI- 10
Db 6 LLLVMGVAMPTHQSQTGFTSVQFPFNGRSMGKPSIAGYHEKRDVEALLSFRKGITL 65

QY 45 SGKAVRLRAAWGAGSCSWEGVGETAGRVVALRLPKRGGLGIIIPSGIGDLHLRYLD 104
Db 66 DPYGLSNWTANNHSHVCLMNGISCPNTNRVVEISLRYGRNLGTLSPYIGNLSLLRLHD 125

QY 105 LSGNSILGVPKSL- 10
Db 126 LSSNALSGRIPAEFGQLKALRIIDLSNNALTSITCIGNGGINGTL- 179

QY 155 TTSG- 155
Db 180 AFSGRIPKELFNCTRLQRIIDLHNSL-TGSIPTSGNCALLQTLNTGPNYLSGSIPTSLA 238
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Db 229 LTVA--INNLOGLIPVFLNMFSSLECLNFGSNQLSGS 263

RESULT 14

Q66CJ0 PRELIMINARY; PRT; 622 AA.

AC Q66CJ0; 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Putative exported protein precursor.

GN ORFNames=YPTB1413;

OS Versinia pseudotuberculosis IP 32953.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Versinia.

OX NCBI_TaxID=273123;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=IP 32953;

RX PubMed=15358858;

RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O., Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin L.V., Brubaker R.R., Fowler J., Hinnbusch B.J., Marceau M., Medigue C., Simonet M., Chenal-Francois V., Souza B., Dacheux D., Elliott J.M., Derbise A., Hauser L.J., Garcia E.;

RA "Insights into the genome evolution of Versinia pestis through whole genome comparison with Versinia pseudotuberculosis.";

RT Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).

RL EMBL; BX936398; CAH20653.1; -.

KW Signal.

FT SIGNAL.

SQ SEQUENCE 1 32 Potential.

SEQUENCE 622 AA; 65230 MW; 30B8C7D77A3D73CD CRC64;

Query Match 14.0%; Score 194; DB 2; Length 622;

Best Local Similarity 26.8%; Pred. No. 3.6e-06;

Matches 68; Conservative 48; Mismatches 78; Indels 60; Gaps 12;

QY 43 NLSGKAVRLRAWVGSCCSWEGVCETASGRVVALRLPKRLGGLIIPSSIGELDLRLY 102

DB 41 NNNNGTINIFDASSNNDIHTLTGLNEL-----LGGF-----SNWL-- 77

QY 103 LDLSGNSLVGEVPSKIQIRLKSITLTDQSILGMS-----SINMLLVSSRRT-L 149

DB 78 IDSHNTINGQSQNNL-VSSDGNNTISAISIGDLGYGAQNNTLINSNNLLIVTQSTII 136

QY 150 DEEPNTISGTNNVSGSNNVSGNDNTVVS-----GNNHVSNNVTVTQSD 198

DB 137 DSDSNTVSGISNNLIESNNII-GNENSCVSDPASPAGAWCDNQNTLIGSDNNTITGAL 195

QY 199 NTVVGSNH---VVSCTKHIVTDNNVSGNDNNVSGSFHTVS-GEHTVSGSNNVTVSGN 254

DB 196 NGLHSHNDIITASSVNNLMDTHNNIAG-----GHYNTISGGGNDIFGSNNVTDST 249

QY 255 HI-VSGSNKVVTDG 267

DB 250 DANINGSNNVVDG 263

RESULT 15

Q75GM9 PRELIMINARY; PRT; 917 AA.

AC Q75GM9; 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein OSJNBa0018K15.10.

GN Name=OSJNBa0018K15.10;

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzeae; Oryza.

OX NCBI_TaxID=39947;

RN [1]

RP SEQUENCE FROM N.A.

RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M., Chao Y.-T., Lee P.-F., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R., Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H., Hsiung J.-N., Hsu C.-H., Kau P.-I., Lee M.-C., Leu H.-L., Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W., Wu H.-P., Shaw J.-F.;

RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AC144737; AAT01367.1; -.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR011009; Kinase_like.

DR InterPro; IPR001611; LRR.

DR InterPro; IPR007090; LRR_plant.

DR InterPro; IPR003591; LRR_typ.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR002290; Ser_thr_kinase.

DR InterPro; IPR001245; Tyr_kinase.

DR Pfam; PF00560; LRR_1; 14.

DR PRINTS; PR00019; LEURICHRPT.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00369; LRR_TYP; 5.

DR SMART; SM00220; S_TK; 1.

DR SMART; SM00219; TyrK; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR ATP-binding; Hypothetical protein.

KW SEQUENCE 917 AA; 96507 MW; AE6DC9F7DD6E0B77 CRC64;

SQ SEQUENCE 14.0%; Score 194; DB 2; Length 917;

Best Local Similarity 26.3%; Pred. No. 5.9e-06;

Matches 81; Conservative 43; Mismatches 108; Indels 76; Gaps 12;

QY 6 AKCCMLLVFLGFIQVAGATSWCHHDDHLALRGLAENLSGKAVRLRAWS--GASCCS 63

DB 4 ATAALLLTALAAAGAV-----NDVLAIVVFKSGVSDPGGV--LAANSEADADACA 56

QY 64 WEGVCETASGRVVALRLPKRLGGLIIP-SSIGELDLRLYLDLSGNSLVGEVPSKIQIRL 122

DB 57 WFGVSCDARAGRDAVALPSAGLSGRLPRLDALLSLALPGNLSGPIPDALPPRA 116

QY 123 KSLTTTDSOSL-----GMGSINN-----LLHVSSRRTLDEEPTISG 158

DB 117 RALDLSANSLSGYLPAAALASCGSLVSLNLSGNLLSGVPDGIWSLPSLRSLDLSGNQLAG 176

QY 159 TNNVSGSG-----SNNVSGNDNTVVS-----GNNHVSNNVTV--V 194

DB 177 ---SVPGGFPFRSSSLRVLDRNLLEGEIPADVGEAGLLKSLDVGHNLFTELPSLRGL 233

QY 195 TGSNDTVVGSNHV-----VSGTKHIVTDNNVSGNDNNVSGSFHTVSGEHTVTS 244

DB 234 TGLSLGAGGNALAGELPGWIGEMAALETLDLSGNRFVGAIPDGISGCKNLVE-----VD 288

QY 245 GSNNTVSG 252

DB 289 LSGNALTG 296

Search completed: October 8, 2005, 02:19:41
Job time : 180 secs

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Db      230 GEIPSGFADEIPEDATVDLSFNQLTGQIPGRVLDNQESFSFG-NPLGCSDH 282
Q69KC3
ID      Q69KC3      PRELIMINARY;      PRT; 1102 AA.
AC      Q69KC3;
DT      25-OCT-2004 (TrEMBLrel. 28, Created)
DT      25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE      Hypothetical protein B1047H05.16.
GN      Name=B1047H05.16;
OS      Oryza sativa (japonica cultivar-group).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC      Ehrhartoideae; Oryzeae; Oryza.
OX      NCBI_TaxID=39947;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Saeki T., Matsumoto T., Katayose Y.;
RT      "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, BAC
RT      clone:B1047H05.";
RL      Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC      -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR      EMBL; AP005966; BAD34184.1; -.
DR      GO; GO:0005224; F:ATP binding; IEA.
DR      GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR      GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR      GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR      InterPro; IPR011009; Kinase_like.
DR      InterPro; IPR001611; LRR.
DR      InterPro; IPR007090; LRR_plant.
DR      InterPro; IPR003591; LRR_Typ.
DR      InterPro; IPR000719; Prot_kinase.
DR      InterPro; IPR002290; Ser_Thr_pkinase.
DR      InterPro; IPR008271; Ser_Thr_pkin_AS.
DR      InterPro; IPR001245; Tyr_pkinase.
DR      Pfam; PF00560; LRR_1; 24.
DR      PRINTS; PR00069; Pkinase; 1.
DR      ProDom; PD000001; Prot_kinase; 1.
DR      SMART; SM00369; LRR_TYP; 7.
DR      SMART; SM00220; S_TKc; 1.
DR      SMART; SM00219; TyrKc; 1.
DR      PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR      PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW      ATP-binding; Hypothetical protein; Kinase;
KW      Serine/threonine-protein kinase; Transferase.
SQ      SEQUENCE 1102 AA; 119984 MW; B960CDE45175C68E CRC64;

Query Match      14.2%; Score 196; DB 2; Length 1102;
Best Local Similarity 24.3%; Pred. No. 5.2e-06;
Matches 84; Conservative 47; Mismatches 109; Indels 106; Gaps 14;

QY      13 VFLGFIQVAGATSWSCHDDHLALRGLAENLSGKGVRLRAAWGASC--CSWEGVGCE 70
Db      19 IFCSISLAICNET-----DDRQALLCFKSQLSGPS--RVLSWSNLSLNFNCWGDVTC 70
QY      71 TAS-GRVALRLPKRG-----QRLKSLTTDS-----LGGIISSIGELDLHRLYLDL 105
Db      71 SRSPPRVIAIDLSSEGITGTISPCLANTLSMTLQLSNNLSHGSIPPKLGLKRLRLNL 130
QY      106 SGNLSGVEVPKSL---QIRKSLTTDS-----QSLG----- 133
Db      131 SNNLSGNTIPSQLSSVQSEIILDSNSFGAIPASLGKCIHQLQDINLNRNQLGRISA 190
QY      134 MGSINML--LHVSRRRLDEEPTNIS-----GTNNSVGSGSNNVVGNDNTVVG 181
Db      191 FGNLSKQLQALVLTNSRLTDEIIPPSLGSSFSRLRVYVDLGNNDITGSIPESLANSSSLQVRL 250
QY      182 NNNHVGSG-----SNNVTVTGSDNTVVGSHVSVGTHKIYTDNNNVVVGNDNNVSGS 232
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Db      251 MSNNLSGVEVPKSLFNTSSLTATFLQONSFGVSGIPAAAMSSPI-----KVISLRDNCISGT 306
QY      233 FHTVSGEHTVTS-----GSNN-----TVSGSNHIVSGSNKV 264
Db      307 IPESLGHIRTLEILTMSVNNLSGLVPPSLFNISLTFLLAMGNNSLV 352

RESULT 13
Q84NG8
ID      Q84NG8      PRELIMINARY;      PRT; 1023 AA.
AC      Q84NG8;
DT      01-JUN-2003 (TrEMBLrel. 24, Created)
DT      01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Putative receptor kinase.
OS      Hordeum vulgare (Barley).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC      Triticeae; Hordeum.
OX      NCBI_TaxID=4513;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Gu Y.Q., Anderson O.D., Londeore C.F., Kong X., Chibbar R.N.,
RA      Lazo G.R.;
RT      "Structural organization of the barley D-hordein locus in comparison
RT      with its orthologous regions of wheat genomes.";
RL      Genome 46:1084-1097(2003).
CC      -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR      EMBL; AY268139; AAP31049.1; -.
DR      GO; GO:0005224; F:ATP binding; IEA.
DR      GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR      GO; GO:0004872; F:receptor activity; IEA.
DR      GO; GO:0016740; F:transferase activity; IEA.
DR      GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR      InterPro; IPR011009; Kinase_like.
DR      InterPro; IPR001611; LRR.
DR      InterPro; IPR007090; LRR_plant.
DR      InterPro; IPR000719; Prot_kinase.
DR      InterPro; IPR008271; Ser_Thr_pkin_AS.
DR      Pfam; PF00560; LRR_1; 17.
DR      PRINTS; PR00019; LEURICHRPT.
DR      ProDom; PD000001; Prot_kinase; 1.
DR      PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN 1.
DR      PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW      ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
KW      Transferase.
SQ      SEQUENCE 1023 AA; 110187 MW; 09EB62D3C41141C6 CRC64;

Query Match      14.1%; Score 195.5; DB 2; Length 1023;
Best Local Similarity 30.3%; Pred. No. 5.2e-06;
Matches 84; Conservative 37; Mismatches 113; Indels 43; Gaps 13;

QY      2 PEYMAKCMMLVFLGFIQVAGATSWSCHDDHLALRGLAENLSGKGVRLRAAW----S 57
Db      5 PWLLRLIALITTTALLHPSTSSSVSTAH-DLPALLSF-KSLITKDPGLGALSSWTNGS 62
QY      58 GASCCSWEGVGCEA-SGRVVALRLPKRGILGIISSIGELDLHRLYLDLSGSLVGEVPK 116
Db      63 THGFCSWTGECCSAHPGHVKALRIQGLGLSGITSPFLNLSRLRALDUSGNKLCQIIPS 122
QY      117 SL-----QIRKSLTTDSQS-----LGMGSINMLLHVSSRRRLDEEPTNISGTNNSVGSGSN 168
Db      123 SIGNCFALRTNLVSNLSGAIPPMGNLSKLL-----VLSVKNDISGTIPTSPAGLA 176
QY      169 NVVSGNDNTVVGSGNNHVG-----SNNVTVTG-----SDNTVVGSHVSVGTHKIYTDNN 219
Db      177 TV-----AVFSVARNHVHGQPPVPMGLNLTALDNLMAADN--IMSGHVPPALLSKLINRS 228
QY      220 NVVSGNDNNVSGSFHTVSGEHTVSGSN---NTVSGS 253
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RN  [1]
RP  SEQUENCE FROM N.A.
RA  Sasaki T., Matsumoto T., Yamamoto K.;
RT  "Oryza sativa nippobare (GA3) genomic DNA, chromosome 7, PAC
RL  clone: P0585H11."
RL  Submitted (NOV-2001) to the EMBL/GenBank/DDAJ databases.
CC  -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR  EMBL; AP004342; BAC20742.1; -.
DR  HSSP; P36897; LIAS.
DR  Gramene; Q8H3W8; -.
DR  GO; GO:0005524; F:ATP binding; IEA.
DR  GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR  GO; GO:0004872; F:receptor activity; IEA.
DR  GO; GO:0016740; F:transferase activity; IEA.
DR  GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR  InterPro; IPR011009; Kinase_like.
DR  InterPro; IPR001611; LRR.
DR  InterPro; IPR007090; LRR_plant.
DR  InterPro; IPR000719; Prot_kinase.
DR  InterPro; IPR008271; Ser_thr_pkin_AS.
DR  Pfam; PF00560; LRR_1; 20.
DR  Pfam; PF00069; Pkinase; 1.
DR  PRINTS; PR00019; LEURICHRPT.
DR  ProDom; PD000001; Prot_kinase; 1.
DR  PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR  PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR  PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR  ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
KW  Transferase.
SQ  SEQUENCE 1010 AA; 109074 MW; 5CCB04E51E18AF02 CRC64;

Query Match 18.9%; Score 262; DB 2; Length 1010;
Best Local Similarity 40.1%; Pred. No. 5.5e-11;
Matches 71; Conservative 19; Mismatches 53; Indels 34; Gaps 5;

QY  7 KCML-LVFLGFLQVAGATSWCHDDHLHALGLAENLS-GKGVRLRAAAGSCCSW 64
DB  8 RCLFSLVALFALLPPPPAAAAPCHPEDLALRAFAGNUSAGGGAGLRAAGSDRCCAW 67
QY  65 EGVGCTASGRVVALRPLKRGIGIIPSSIGELDHLRYLDLSGNSIVGVPKSLQIRLKS 124
DB  68 DGVACD-AAARVTLALPGRGLEGPPIPSLAALRLQDLDSHNAIT----- 113
QY  125 LTTDSQSLGWSINMLLVSSRRTLDEEPTISGT-----NNSVSGSNVNVSG 173
DB  114 -----GGISALLAAVSLRTANLSSNLLNDTLDLAALPHLSAFNASNLSLG 160

RESULT 3
QYFN37 PRELIMINARY; PRT; 1036 AA.
AC QYFN37
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Putative receptor protein kinase.
GN Name=At5g53890;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98162728; PubMed-9501997;
RA Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. III.
RT Sequence features of the regions of 1,191,918 bp covered by seventeen
RT physically assigned pl clones."
RL DNA Res. 4:401-414 (1997).
RN [2]
RP SEQUENCE FROM N.A.

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RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DDAJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA Tang J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
RA Davis R.W., Ecker J.R., Theologis A.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDAJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AB007644; BAB10719.1; -.
DR EMBL; AY064019; AAL36375.1; -.
DR EMBL; AY091180; AAM14119.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007090; LRR_plant.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00560; LRR_1; 19.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
KW Transferase.
SQ SEQUENCE 1036 AA; 114339 MW; 6DF9511FC2A4E261 CRC64;

Query Match 18.7%; Score 258.5; DB 2; Length 1036;
Best Local Similarity 30.7%; Pred. No. 1e-10;
Matches 89; Conservative 50; Mismatches 98; Indels 53; Gaps 14;

QY 10 MLLVFLGFLQVAGATSWCHDDHLHALGLAENLSGKGVRLRAAW-SGASCCSWEGVG 68
DB 5 LLLVFF-----VGSSVSQCPNDLSALRELALGNKSVTE---SWLNGSRCCWDGVF 56
QY 69 CE--TASGRVALRPLKRGIGIIPSSIGELDHLRYLDLSGNSIVGVEPKSL-----QIRL 122
DB 57 CEGSDVSGRVTKLVLPKLEGVISKIGELTELRLVLDLSRNLKGEVPAETSKLEQLQV 116
QY 123 KSLTDSQSLGMSI-NMLLVSSRRTLDEEPTISGTNNVSG-----SGSNVNVSG 173
DB 117 LDL---SHNLLSGVLGVVSGKLKIQSLNISNSLSGKLSLDVGFPLVNLVNSNLFEG 173
QY 174 NDNTVV---SGNNNHVSGSNNTVVTGSDNTVVGSNHHVSGTKHIVTDNNNVWSG----- 224
DB 174 EIHPELCSSGGIQLVLDLNMRLVGNLD---GLYCNCKSIQQLHDSNRLTQQLPDYLY 229
QY 225 -----NDNNVSGSFHTVSGEHNVTGSGNNVTGSGNNHVSNGSNK---VWTD 266
DB 230 SIRELEQLSISGNY--LSGE---LSKNLSNLSGLSKLLISENRFSDVIPD 274

RESULT 4
QY3UH1 PRELIMINARY; PRT; 1124 AA.
ID Q63UH1
AC Q63UH1;

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 8, 2005, 02:01:21 ; Search time 176 Seconds
(without alignments)

Title: US-10-657-852B-15
Perfect score: 1385
Sequence: 1 MPEYNAKCCMLLVFLGLFIQ.....NTVSGSNHIVSGSNKQWTDG 267

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

```
Database :      UniProt_03:*
          1: uniprot_sprot:*
          2: uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	%			DB	ID	Description
		Score	Match	Length			
1	530	38.3	118	2	Q9M3W4	Q9m3w4 lolium pere	
2	262	18.9	1010	2	Q8H3W8	Q8h3w8 oryza sativ	
3	258.5	18.7	1036	2	Q9fn37	Q9fn37 arabidopsis	
4	221.5	16.0	1124	2	Q63UH1	Q63uh1 burkholderi	
5	218	15.7	1012	2	Q62KN5	Q62kn5 burkholderi	
6	212	15.3	353	2	Q9ZNX4	Q9znx4 petunia hyb	
7	204	14.7	1021	1	PSKR_DRUCA	Q81pb4 daucus caro	
8	201	14.5	1065	2	Q66QA4	Q66qa4 oryza sativ	
9	199.5	14.4	784	2	Q9C9H6	Q9c9h6 arabidopsis	
10	197.5	14.3	751	2	Q940M7	Q940m7 arabidopsis	
11	197.5	14.3	751	2	Q9FGQ5	Q9fgq5 arabidopsis	
12	196	14.2	1102	2	Q69KC3	Q69kc3 oryza sativ	
13	195.5	14.1	1023	2	Q84NG8	Q84ng8 hordeum vul	
14	194	14.0	622	2	Q66CJ0	Q66cj0 yersinia ps	
15	194	14.0	917	2	Q75GM9	Q75gm9 oryza sativ	
16	194	14.0	1063	2	Q67IT7	Q67it7 oryza sativ	
17	193.5	14.0	372	2	Q89J37	Q89j37 bradyrhizob	
18	192.5	13.9	846	2	Q9C9H7	Q9c9h7 arabidopsis	
19	192	13.9	727	2	Q67TW5	Q67tw5 oryza sativ	
20	192	13.9	1060	2	Q6ZGM3	Q6zgm3 oryza sativ	
21	190.5	13.8	943	2	Q9SRL7	Q9srl7 arabidopsis	
22	190.5	13.8	1008	1	PSKR_ARAPH7	Q9zvr7 arabidopsis	
23	190	13.7	622	2	Q8ZGB5	Q8zgb5 yersinia pe	
24	189.5	13.7	605	2	Q6K9D3	Q6k9d3 oryza sativ	
25	188.5	13.6	922	2	Q91P64	Q91p64 moraxella c	
26	188.5	13.6	1011	2	Q6Z0A9	Q6z0a9 oryza sativ	
27	187.5	13.5	784	2	Q9L579	Q9l579 arabidopsis	
28	186.5	13.5	465	2	Q814Z3	Q814z3 plasmodium	
29	186	13.4	641	2	Q9LDG0	Q9ldg0 oryza sativ	
30	186	13.4	645	2	Q9SVN1	Q9svn1 arabidopsis	
31	185	13.4	1012	2	Q7XPI3	Q7xpi3 oryza sativ	

ALIGNMENTS

RESULT 1

Q9M3W4	PRELIMINARY;	PRT;	118 AA.
ID	Q9M3W4		
AC	Q9M3W4;		
DT	01-OCT-2000 (TrEMBLrel. 15, Created)		
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	Ice recrystallisation inhibition protein (Fragment) .		
OS	Lolium perenne (perennial ryegrass) .		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;		
OC	Poaceae; Lolium.		
NCBI_TaxID=4522;			
[1]			
RN			
RP	SEQUENCE FROM N.A.		
RA	Sidebottom C.M.;		
RL	Thesis (1999), University of York.		

RESULT 2

Q8H3W8	Q8H3W8	PRELIMINARY;	PRT; 1010 AA.
ID	Q8H3W8		
AC	Q8H3W8;		
DT	01-MAR-2003 (T-EMBLrel. 23, Created)		
DT	01-MAR-2003 (T-EMBLrel. 23, Last sequence update)		
DT	01-MAR-2004 (T-EMBLrel. 26, Last annotation update)		
DE	Putative phytoosulfoligine receptor.		
GN	Name=P0585H11.109;		
OS	Oryza sativa (japonica cultivar-group).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
OC	Ehrhartoideae; Oryzaceae;		
OC	NCBI TaxID=39947;		

A:Cross-references: UNIPROT:Q22178; EMBL:AC002391; NID:G2642427; PID:G2642433
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: A84623
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-773 <STO>
A:Cross-references: GB:AE002093; NID:G2642433; PIDN:AAB87101.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g23300; T20D16.7
A:Map position: 2
A:Introns: 545/1
C:Superfamily: protein kinase homology

Query Match 11.7%; Score 162; DB 2; Length 773;
Best Local Similarity 27.3%; Pred. No. 0.00028;
Matches 66; Conservative 36; Mismatches 86; Indels 54; Gaps 8;

QY 26 SMSCHDDHLALRGLAENLSGKGAVALRAAWGASCCSMEGVGCEATASGRVVALRLPKRG 85
DB 55 SNNYDHD-----NPCSRRGVLNNDSS-RVVTLSLPNSN 86

QY 86 LGGIIPSSIGELDHRLYDLGNSLGVGPKSL---QIRLKSLLTDSQS---LGMGSI 137
DB 87 LVGSIPLDGLFQNLQSLNNSLNGSLPVEFFAADKLRLFLDLSNNLSIGEIPVSIIGL 146

QY 138 NMLLHVSRRTLDDEPNTTSGTNNVSGSNNVSGNDNTVSGNNHVVSGNNVTVTGS 197
DB 147 HNL-----QTLNLSNIIFTGKLPA-----NLASLSLTSVSLKNVYSGEFPFGGGRS 194

QY 198 DNTVGSNNHVST--KHIVTNNVSGNDNNVSGSFHTVSG---EHTVSGSNNVTS 251
DB 195 VQYLDISSNLNGSLPPDFSGDNLRLYNVSYNQISGEIPNPVAGGPPQATVDFSFNNLT 254

QY 252 GS 253
DB 255 GS 256

RESULT 15
T00475
N:Alternate names: hypothetical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T00475; F84762
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, April 1998
A:Description: Arabidopsis thaliana chromosome II BAC F1913 genomic sequence.
A:Reference number: Z14160
A:Accession: T00475
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-905 <ROU>
A:Cross-references: UNIPROT:O64757; EMBL:AC004238; NID:G3033373; PID:G3033389
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: F84762
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-905 <STO>
A:Cross-references: GB:AE002093; NID:G3033389; PIDN:AAC12833.1; GSPDB:GN00139
C:Genetics:

A:Gene: F1913.16; At2g34930
A:Map position: 2

Query Match 11.7%; Score 161.5; DB 2; Length 905;
Best Local Similarity 23.1%; Pred. No. 0.00037;
Matches 88; Conservative 45; Mismatches 105; Indels 143; Gaps 16;

QY 10 MLLVFLGFLQVAGATSNCHHDDLHAL---RGLAENLSGKGAVALRAAWGASCCSMEG 66
DB 14 LILILLKNNLVGSAASPKCISTEQALLTFRALTDLSSR-----LFSWSGPDCCNWP 68

QY 67 VGCETASGRVVA--LRLP-----KRG--LGGI----- 89
DB 69 VLCDARTSHVVKIDLRNFSQDVRSDEYKRGSLRGKIHPSLTQLKFLSYLDLSSNDFNEU 128

QY 90 IPSSIGELDHRLYDLGNSLGVGPKSL-----QIR- 121
DB 129 IPEFIGQIVSLRYLNLSSSFSGEIPTSLGNLSKLESLLDYAESFGDSCTLSLRASNLRW 188

QY 122 LKSLTTDSQSLSGMSINML-----LHVSSRRTLDEBPNTISG----- 158
DB 189 LSSLSLSUKYLMGVNLSGAGETWQDFSRISALKELHFNSE-LKNLPPTLSSADLK 247

QY 159 -----TNNVSGSNNVSGNDN-----TVVSGNNN-----HVSNNNTV 193
DB 248 LLEVLDSLNSLNSIPNWLFGLTNLRKFLRWDFLQSGIPTGFKNLKLETLDSLNNLA 307

QY 194 VTGSNTVVG-----SNHVSGTKHIVTDNNNVVSGN-----DNNVSGSFHT 235
DB 308 LQGEIPSVLGDLPQLKFLDLSANELNGQTHGFDAFSRNKGNLSVFLDLSNKLGLTPE 367

QY 236 VSG---EHTVSGSNNVTVSGS 253
DB 368 SLGSLRNLTDLSSNSFTGS 388

Search completed: October 8, 2005, 02:20:26
Job time : 43 secs

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: H84421

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-716 <STO>

A;Cross-references: UNIPROT:Q9ZU46; GB:AE002093; NID:94262228; PIDN:AAD14521.1; GSPDB:GN

C;Genetics:

A;Gene: At2g01210

A;Map position: 2

Query Match 11.9%; Score 164.5; DB 2; Length 716;

Best Local Similarity 27.4%; Pred. No. 0.00017;

Matches 63; Conservative 34; Mismatches 78; Indels 55; Gaps 9;

QY 10 MLLVFLGFTLVAGATSWSCHDDHALRGLAENLSGKGAVALRAAW--SGASCCSWEV 67

Db 1 MLASLIIFVALLCNVTVISGLNDEGFALLTFKQSVHDDPTGSLN-NNNSDENACSWNGV 59

QY 68 GCBTASGRVVALRPLKRGIGIIPSSIGELDLRLYLDLSGNSLVGEVP-----KSL 118

Db 60 TKCEL--RVVSLIPRKNLYGSLPSSLGFLSSLRHLNRSNRPYGSLSLPQLPHLQGLSL 117

QY 119 QI-----RLKSLTT--DSQSLGMSINM-LLHVSRRRTLDEEPTISGT-- 159

Db 118 VLYGNSFDGSLSEIEGKLKLTQTLQSLNLFNGSLPLSLIQCNRKLTLDVSRNLSGPLP 177

QY 160 -----NNSVGSGNNVSGNDNTVVSGNNNVSGS 189

Db 178 DFGSFAVSLKLDLAFNQFNGSIPSDIGNL--SNLQGTADFSHNHFTGS 225

RESULT 12

B85440

receptor kinase-like protein [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Aug-2004

C;Accession: B85440

R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999

A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A;Reference number: A85001; MUID:20083488; PMID:10617198

A;Accession: B85440

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-766 <STO>

A;Cross-references: UNIPROT:O23161; GB:NC_001268; NID:g7270708; PIDN:CAB80391.1; GSPDB:G

C;Genetics:

A;Gene: AT4g37250

A;Map position: 4

C;Superfamily: protein kinase homology

Query Match 11.8%; Score 164; DB 2; Length 766;

Best Local Similarity 28.5%; Pred. No. 0.0002;

Matches 63; Conservative 35; Mismatches 67; Indels 56; Gaps 9;

QY 60 SCCSVCVCETASGRVALRPLKRGIGIIPSSIGELDLRLYLDLSGNSLVGEVPKSL- 118

Db 51 SPCSWRGICNNDS-KVLTLSLPNSQLGSLIPSDLSGLTLQLDLNNSFNGPLPVSF 109

QY 119 ---QIRKLKSLTDSQS---LGMGSINMLHVSRRRTLDEEPTISGTNNVSGSGNNVV 171

Db 110 NARELRFDLSSNNWISGEIPSAIGDLHNL-----TLNLSDNALA-----GKLPNTLA 157

QY 172 SGNDNTVVSGNNHVSNNVTVTGSDNTVVGSHVSGTKHIVTNNNVVSG----- 224

Db 158 SLRNLTVVSLNNYFSGE-----IPGWRVV---EFLDLSSNLINGSLLPPDFG 202

QY 225 --NDNVSGSFHTVSGE-----HNTVSGSNNTVSG 252

Db 203 GYSLOYLVNSFVNQISGEIPPEIGVNPFRNVTVDLSFNLTG 243

RESULT 13

T05322

hypothetical protein F18F4.240 - Arabidopsis thaliana

N;Alternate names: hypothetical protein F1C12.60

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Accession: T05322; T04898

R;Bevan, M.; Terry, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; De ewes, H.W.; Mayer, K.F.X.; Schueller, C.

submitted to the Protein Sequence Database, April 1998

A;Reference number: Z15408

A;Accession: T05322

A;Molecule type: DNA

A;Residues: 1-1232 <BEV>

A;Cross-references: UNIPROT:Q9SN91; EMBL:AL022224

A;Experimental source: cultivar Columbia; BAC clone F1C12

R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.

submitted to the Protein Sequence Database, February 1998

A;Reference number: Z15388

A;Accession: T04898

A;Molecule type: DNA

A;Residues: 1-305 <BEW>

A;Cross-references: EMBL:AL021637

A;Experimental source: cultivar Columbia; BAC clone F18F4

C;Genetics:

A;Map position: 4

A;Introns: 863/1; 1116/1

A;Note: F1C12.60; F18F4.240

C;Superfamily: protein kinase Xa21; leucine-rich alpha-2-glycoprotein repeat homology;

Query Match 11.7%; Score 162.5; DB 2; Length 1232;

Best Local Similarity 25.3%; Pred. No. 0.00045;

Matches 71; Conservative 41; Mismatches 94; Indels 75; Gaps 11;

QY 11 LLVFLGFTLVAGATSWSCHDDHAL-----RCLAENLSGKGAVALRAAWS--GASCCSW 64

Db 4 LVLLLLFLLCFSGLGQFGIINDDQLTLLVKKSLVTNPQEDDPLR---QWNSNINVCSS 60

QY 65 EGVGCB-TASGRVALRPLKRGIGIIPSSIGELDLRLYLDLSGNSLVGEVPKSLQIRLK 123

Db 61 TGVTCNTGLFRVIALNLTLGLTGSISPFWGFDFNLHLDLSSNLVGPITALS-NLT 119

QY 124 SLTTSQSLGMSINMLHVSRRRTLDEEPTISGTNN--SVGSGSNVNVSGNDNTVVSG 181

Db 120 SLES-----LFLFSNQLTGEIPSQLGSLVNIRSLRIGDNELVGDIPETL--G 164

QY 182 N-----NNHVS-----SNTVTGSD 198

Db 165 NLVNLQMLALASCLRTGPIPSQLGRIVVQSILIQNLYLEGPIPAELGNCSDLTIVFTAAE 224

QY 199 NTVVGSHVVSGETKHIVTNNNVSGNDNNVSGSFHTVSGE 239

Db 225 NMLNGTIPAEGR-----LENELNLANNSLTGEIPSQLGE 261

RESULT 14

T00502

probable receptor-like protein kinase At-2g23300 [imported] - Arabidopsis thaliana

N;Alternate names: protein kinase homolog T2016.7

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 16-Aug-2004

C;Accession: T00502; A84623

R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kau

submitted to the EMBL Data Library, November 1997

A;Description: Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence.

A;Reference number: Z14164

A;Accession: T00502

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-773 <ROU>

C:Accession: G84524
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: G84524
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-983 <STO>
A:Cross-references: UNIPROT:Q9ZUK3; GB:AE002093; NID:g4115363; PIDN:AAD03365.1; GSPDB:GN
C:Genetics:
A:Gene: At2g15080
A:Map position: 2

Query Match 13.0%; Score 179.5; DB 2; Length 983;
Best Local Similarity 21.7%; Pred. No. 1.9e-05;
Matches 81; Conservative 56; Mismatches 113; Indels 123; Gaps 14;

QY 1 MPEYMAKCCMLLVFLGFILOVAGATSWSCHHDDLHAL-----RGLAENLSKGAVRLR 53
DB 2 MKGYITLSFLIILIFNLFDEFAASTRHLCDDPDQSDAILFEKNEFETLESCEFDSNIPKLT 61

QY 54 AAWSGAS-CCSWEVGVCETASGRVVAL-----RLP----- 82
DB 62 ESWTNSDCYWDGIKDAKFGDVIELDSFSCRLGQNSNSLFLPQLRFLTTLDLSN 121

QY 83 -----KRGLGIIPISSIGELDHLRYLDLSGNSLVEGPKSIQ 119
DB 122 NDFIQIPISSLETLSNLTLDLSRNHFSGRIPSSIGNLSHLIFVDFSHNFFSQIPSSLG 181

QY 120 IRKSLTTDSQSL-----GMGSINML--LHVSRRTLDEEPTISG----- 158
DB 182 Y-LSHLTSPNLSYNNFSGRVPSSIGNLSYLTTLRLSRNFFGGLPSSGLFHLTDLILD 240

QY 159 TNNVSGSGNNVSGNDNTVSGNNHNVSGNNVTGSDNTVSGNHVVG-----TKH 213
DB 241 THNFVKIPSSL-----GNLSHL-----TSIDLHKNFVGIPIPSGLNLSCLTTF 285

QY 214 IVTDNN-----NVSGNDNNVSGSFHTV---SGEHTVSGNNVTSGS--- 253
DB 286 ILSDDNIVGEIPSGFNGNLQDLILNVKNSKLSGFPFIALNLRLKLTSLIFNNLTGLTP 345

QY 254 NHIVSGSNKVVD 266
DB 346 SNMSSLNLKLF 358

RESULT 6
C84633
probable disease resistance protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana [mouse-ear cress]
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: C84633
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: C84633
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-743 <STO>
A:Cross-references: UNIPROT:Q9ZUH7; GB:AE002093; NID:g4115376; PIDN:AAD03377.1; GSPDB:GN
C:Genetics:
A:Gene: At2g24160
A:Map position: 2

Query Match 12.7%; Score 176.5; DB 2; Length 743;
Best Local Similarity 26.7%; Pred. No. 2.3e-05;
Matches 63; Conservative 35; Mismatches 81; Indels 57; Gaps 10;

QY 55 AWSGAS-CCSWEVGVCETASGRVVALRL-----PKRG-----LG 87
DB 11 SNKSSDCSWSVTCDAKYGVVISLLGVNLNNTLKNSGLFKLOYLQNLTLRYCNLY 70

QY 88 GIPISSIGELDHLRYLDLSGNSLVEGPKS-----LQIRKSLTTDSQSLGMSIN 138
DB 71 GEIPFSLGTLSHLTFLDLSENKLVGVQVPSISIGNLTCLMYLRLSINHLSGKS-SVSPANLT 129

QY 139 MLLHVSSRRTLDEEPTI---SGTNNVSGSGNNVSGNDNTVVS-----GNNN 184
DB 130 KLIQIDIREN-DFEPELIPDMRFHNLFGFGNGFFGPTSLFTIPSLRWVNLDRSNN 188

QY 185 ---HVSGSNNTVVTGSDNTVWGSNVHVSCTKHIVTDNNNV--SGMNNVSGSFHT 235
DB 189 FTGHIDFGNSSLSRSLSYLSLADNFPDGPPIPEISIKFLNLVLLDLRNSFGGFPT 244

RESULT 7
B86440
probable protein kinase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana [mouse-ear cress]
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: B86440
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzalli
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: B86440
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-590 <STO>
A:Cross-references: UNIPROT:Q9C867; GB:AE005172; NID:g11054670; PIDN:AAG27890.1; GSPDB:
C:Genetics:
A:Map position: 1

Query Match 12.5%; Score 173.5; DB 2; Length 590;
Best Local Similarity 24.7%; Pred. No. 2.8e-05;
Matches 70; Conservative 44; Mismatches 90; Indels 79; Gaps 13;

QY 5 MAKCCMLLVFLGFILOVAGATSWSCHHDDLHALRGLAENLSKGAVRLRAA----- 55
DB 6 MKSCCSWLLLSILCSLSNESQ-----AISPDGEALLSFRNAVTRSDSFH 51

QY 56 -W-SGASCCSWEVGVCETASGRVVALRLPKRGLGIIPISSIGELDHLRYLDLSGNSLVG 112
DB 52 QWRPEPDPCNNWGVTCDAKTRVITLNTYHKIMGPLPDPDGKLDHLRLMLHNNALYG 111

QY 113 EYPKSL-----QIRLKS-LTTDSQSLGMSINMLLVSSRRTLDEEPTISG----- 158
DB 112 AIPTALGNCTALEEHLQSNYFTGPIPAEMGDPLGL-----QKLDMSNTLSGPIPASL 165

QY 159 -----TNNVSGSGNNVVSNGN--DNTVVSNGNNHNVSGNNVTGSDNTVWGSNVSG 210
DB 166 GQLKLSNFNV---SNNFLVGGIIPSDGVLSG-----FSKNSFIGNLNLG- 207

QY 211 TKHIVTDNNNVSGMNNVSGSFHTVSGEHTVSGNNVTSGS 253
DB 208 -KHV-----DVVQDDSG-NPSSHSGQGNQKNSGKLLISAS 243

RESULT 8
AE1857
hypothetical protein al10406 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

R.Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
 geno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AF0169
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-622 <KUR>
 A:Cross-references: UNIPROT:O8ZGB5; GB:AL590842; PIDN:CAC90217.1; PID:g15979437; GSPDB:G
 C:Genetics:
 A:Gene: YPO1388

Query Match 13.7%; Score 190; DB 2; Length 622;
 Best Local Similarity 26.3%; Pred. No. 1.8e-06;
 Matches 68; Conservative 49; Mismatches 72; Indels 70; Gaps 13;

QY 43 NLGKGAFLRAAWGSCCSWEGVGCETASGRVVALRPLKGLGILPSSIGELDLHRY 102
 DB 41 NNGNGTINFASNNNDIHTLTGLNEQ-----LGGF-----SNHL-- 77

QY 103 LLDLGNLSVGEVPEKSLQIRLKLITDSQ-----SLGMG-----SINMLHVS 145
 DB 78 IDSHNTIDGGQSNL-----VSDGNMISALSLDGLFYGAQNTLNNSNNLLIVTQ 131

QY 146 RRT-LDEEPTISGTNNVSGSNNVSGNDNTVVS-----GNNHVSNNNTV 193
 DB 132 GSTIIDSNTVSGISNNLIESNNII-GNENSCYSDPASPGAWCVDNQNTLIGSDNNT 190

QY 194 VTGSDNTVVSNNH--VVSSTKHIVTDNNVSGNDNNVSGSFHTVS-GEHNTVSGSNNNT 249
 DB 191 ITGALNGLNLSHNDIIASVNNLMDTHNNIAG-----GHYNTISGGNNDIFGSENN 244

QY 250 VSGSNHI-VSGSNKVVTDG 267
 DB 245 VTDSNTANINGSNNYVDG 263

RESULT 3
 T05251
 probable disease resistance protein F18A5.210 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C:Accession: T05251
 R:Bevan, M.; Weber, N.; Grueninger, D.; Schmidheini, T.; Bancroft, I.; Mewes, H.W.; Maye
 submitted to the Protein Sequence Database, February 1999
 A:Reference number: Z15405
 A:Accession: T05251
 A:Molecule type: DNA
 A:Residues: 1-645 <BEV>
 A:Cross-references: UNIPROT:Q9SVN1; EMBL:AL035528
 A:Experimental source: cultivar Columbia; BAC clone F18A5
 C:Genetics:
 A:Map position: 4
 A:Introns: 216/1; 541/1
 A:Note: F18A5.210

Query Match 13.4%; Score 186; DB 2; Length 645;
 Best Local Similarity 22.1%; Pred. No. 3.8e-06;
 Matches 82; Conservative 46; Mismatches 115; Indels 128; Gaps 14;

QY 9 CMLLVFLGFILOVAGATSWSCCHDDHLALRGLAE-----NLGKGAFLRAAW-SGAS 60
 DB 7 CLILSLNSKVLASHVGHLCROQKNALLEFKNQEFVHEFNSNGIVGVKTEKWRNNTD 66

QY 61 CCSWEGVGCETASGRVVALR-----PKR-----GLGILPSSI 94
 DB 67 CCSWDGISCDPKTKGVKVELDLNMSFLNGPLRYDSSILFRLOHLNLDLGSNNFSGILPDSI 126

QY 95 GELDHLRYLDLGSNLVGEVPEKSLQIRLKLSTTDSQSL-----GMGSINML--LHV 143
 DB 127 GSKYLRLVSLGDCNLFKGIPISSLG-NLTYLTNLDLSVNDFTGELPDSMGHLNKLTELHL 185

QY 144 SSRTLDDEEPTISGTN--NSVSGSN-----NVVSGN-----DN 176
 DB 186 GSAKLSGNFPMLNLSELTLIDLSNOFGENQTYLDISANKIGQVPOWLKSLPEL 245

QY 177 TVVSGNNHVS-----SNNTVVTGSDNTVVS 204
 DB 246 QYVNISQNSFSGFEGPADVIQRCGELLMLDISSNTFFQDPFLLPNSTIFLGSNDNRFSGE 305

QY 205 -----NHVVSGTKHIVTNN-----NVVSGNDNNVSGSF--HTVSGEHN 241
 DB 306 IPKTIKLVSLDTLVLSNNFNNGSIPRCFEKFNFTTSLVHLRNNLNLGEPPEESIDHUR 365

QY 242 TVSGSNNNTVSG 252
 DB 366 SLDVGRNRLSG 376

RESULT 4
 T46070
 hypothetical protein T18N14.120 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 16-Aug-2004
 C:Accession: T46070
 R:Delserny, M.; Berger, C.; Cooke, R.; Grellert, F.; Laudie, M.; Mewes, H.W.; Lemcke, K.;
 submitted to the Protein Sequence Database, December 1999
 A:Reference number: Z23013
 A:Accession: T46070
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-836
 A:Cross-references: UNIPROT:Q9SCT4; EMBL:AL132968
 A:Experimental source: cultivar Columbia; BAC clone T18N14
 C:Genetics:
 A:Map position: 3
 A:Introns: 625/1
 A:Note: T18N14.120
 C:Superfamily: protein kinase homology

Query Match 13.3%; Score 184.5; DB 2; Length 836;
 Best Local Similarity 25.7%; Pred. No. 6.7e-06;
 Matches 82; Conservative 48; Mismatches 100; Indels 89; Gaps 15;

QY 10 MLLVFLGFILOV-----AGATSW-----SCHDDHLALRGLAENLKGKGAFLRAAWSG 58
 DB 22 LLLCFLLPQAQVAGGGGSHSDGIVVTQYQALQAIKHELIDFTG-----VLKSWNN 76

QY 59 AS-----CCSWEGVGCETASGRVVALRPLKRGILGGIIPSSIGELDLHRYLDLGSNLVGEV 114
 DB 77 SASSQVCSGAGIKC--LRGQVVAIQLPWKGLGGTISEKIGQLGSLRKLHLNNVIAGSV 134

QY 115 PKSLQIRLKL-----TTDSQSLGMSINMLHVSRRITLDEEPTISGT----- 159
 DB 135 PRSLGY-LKSLRGVYLFNNRLSGSIPVSLGNCPLL-----QNLDSLNLGTGAIPTT 187

QY 160 -----NNSVSGSNNVSGNDNTVVSNNHVSNNVSGS--NNTVVTGS-----D 198
 DB 188 ESTRLRYLNLSPNSLSGPLPVSVARSYTLTFDLQHNNLSGSIPIPFVNGSHPLKTLNLD 247

QY 199 NTVVSGSNHVSSTKHIVTNNVSGNDNNVSGNSGFSHTVSG-----EHTVSGS-- 246
 DB 248 HNRFGSAPVSLCKHSLLEE---VSLSHNLQSSIPRECGLPLHQSLDYSYNGTIP 304

QY 247 -----NNTVS---GSNHI 256
 DB 305 DSFSNLSLVSLSNLSNHL 323

RESULT 5
 G84524
 probable disease resistance protein [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 8, 2005, 02:09:36 ; Search time 41 Seconds
(without alignments)
626.582 Million cell updates/sec

Title: US-10-657-852B-15
Perfect score: 1385
Sequence: 1 MPEYMAKCMMLVFLGLIQ.....NTVSGSNHIVSGSNKVVTDG 267

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: Pirl:*
2: Pirl2:*
3: Pirl3:*
4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	190.5	13.8	1008	D84434	probable receptor-
2	190	13.7	622	AF0169	probable exported
3	186	13.4	645	T05251	probable disease r
4	184.5	13.3	836	T46070	hypothetical prote
5	179.5	13.0	983	G84524	probable disease r
6	176.5	12.7	743	C84633	probable disease r
7	173.5	12.5	590	B86440	probable protein k
8	169	12.2	420	AE1857	hypothetical prote
9	168.5	12.2	1095	G96746	hypothetical prote
10	168	12.1	1019	C96519	probable disease r
11	164.5	11.9	716	H84421	probable receptor-
12	164	11.8	766	B85440	receptor kinase-li
13	162.5	11.7	1232	T05322	hypothetical prote
14	162	11.7	773	T00502	probable receptor-
15	161.5	11.7	905	T00475	probable disease r
16	161	11.6	719	T47727	hypothetical prote
17	161	11.6	907	A86460	99.9K hypothetical
18	159.5	11.5	768	T17462	disease resistance
19	158.5	11.4	658	B84664	probable receptor-
20	158	11.4	478	H86459	hypothetical prote
21	157.5	11.4	996	T10725	protein kinase Xa2
22	157	11.3	241	S61925	cyst wall protein
23	156.5	11.3	702	A86383	76.4K protein kina
24	156.5	11.3	876	D96558	probable protein k
25	156	11.3	371	T49908	hypothetical prote
26	156	11.3	638	T05606	protein kinase hom
27	155.5	11.2	942	1 JQ1674	protein kinase TMK
28	155	11.2	729	F86308	Similar to disease
29	154.5	11.2	1143	T10636	hypothetical prote

30	154	11.1	720	2	T02361	hypothetical prote
31	153	11.0	668	2	T05257	probable disease r
32	152.5	11.0	646	2	B84852	probable receptor-
33	152.5	11.0	655	2	G96524	protein Tln15.9 [i
34	152.5	11.0	838	2	A96557	probable receptor-
35	152.5	11.0	980	2	H84632	probable disease r
36	151.5	10.9	480	2	T00971	probable protein k
37	151	10.9	693	2	F96557	hypothetical prote
38	151	10.9	863	2	F85343	receptor protein k
39	151	10.9	981	2	T50851	leucine-rich repea
40	150.5	10.9	221	2	T07079	probable receptor-
41	150.5	10.9	672	2	B84782	protein kinase Xa2
42	150.5	10.9	813	2	T04313	sericin MG-2 - gre
43	149.5	10.8	286	2	C61615	probable receptor-
44	149.5	10.8	645	2	E96631	probable receptor-
45	149	10.8	976	2	B84659	probable receptor-

ALIGNMENTS

RESULT 1

D84434
probable receptor-like protein kinase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: D84434
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: D84434
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1008 <STO>
A:Cross-references: GB:AE002093; NID:96598459; PIDN:AAC78507.2; GSPDB:GN00139
C:Genetics:
A:Gene: At2g02220
A:Map position: 2

Query Match 13.8%; Score 190.5; DB 2; Length 1008;

Best Local Similarity 27.5%; Pred. No. 3e-06; Matches 68; Conservative 45; Mismatches 93; Indels 41; Gaps 12;

QY 9 CMLLVFLG---FILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSW 64

Db 7 CVIVIFLTLLCFFYSSQTTSRCHPHDLEALRDFIAHLEPKPDGWINSS-SSTDCNW 65

QY 65 EGVGGET-ASGRVVALRLPKRGGLIIPSSIGELDLHLRYLDLSGNSLVGEVPSKLOIRLK 123

Db 66 TGITCNNTTGRVIRLELGNKKLSGLKSLGKLDLIRVLNLSRNFKDISPLSI-FNLK 124

QY 124 SLTT---DSQSLGMSINLLHVSSRRTLDEPNTISGT-----NNS-----VGSGSNV 170

Db 125 NIOTLDLSSNDLS-GGIPTSINLPALQSPDLSSNKFNGSLPSHICHNSTQIRVVKLAVNY 183

QY 171 VSGNDNTVVSNNHVSNNVTVTGSDNTVVSNNHVSQTKHIVTD-----NNNVVSGN 225

Db 184 FAG-----NFTSGFGKCVLL---EHLCLGMNDL---TGNIPEDLFLKRLNLGIQ 228

QY 226 DNNVSGS 232

Db 229 ENRLSGS 235

RESULT 2

AF0169

probable exported protein YP01388 [imported] - Yersinia pestis (strain CO92)

C:Species: Yersinia pestis

C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C:Accession: AF0169

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PD 18-MAR-2004.
XX
PF 09-SEP-2003; 2003WO-NZ000199.
XX
PR 09-SEP-2002; 2002US-0409557P.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX (WRIG-) WRIGHTSON SEEDS LTD.
XX
PI Demmer J, Shenk MA, Hall C, Fish SA;
XX WPI; 2004-248453/23.
DR N-PSDB; ADM41458.
XX
PT New antifreeze proteins and encoding polynucleotides, useful for
PT modulating cold tolerance in organisms, as food additives, or for
PT treating tumors or disorders associated with the presence of unwanted
PT biocrystals (e.g. gout).
XX
PS Claim 7; SEQ ID NO 14; 71pp; English.
XX
CC The present sequence is that of APE1, an antifreeze protein of perennial
CC ryegrass. The encoding cDNA was isolated from a pseudostem cDNA
CC expression library. The invention provides forage grass (perennial
CC ryegrass and tall fescue) antifreeze proteins and the polynucleotides
CC encoding them ADM41458-ADM41483. The polynucleotides were isolated from
CC tissues taken at different times of year (winter and spring) and from
CC different parts of the plants. The polynucleotides can be used to
CC modulate the cold tolerance of an organism, especially plants, mammals,
CC insects, fungi, archaea and bacteria. The method involves incorporating
CC an antifreeze polynucleotide, under the control of a gene promoter
CC sequence, into the genome of the organism, or introducing double-stranded
CC RNA corresponding to the polynucleotide into the cells of the organism,
CC thereby inhibiting expression of an antifreeze polypeptide. The
CC antifreeze protein can be used for the cryopreservation of a cell or
CC tissue, as a food additive of a frozen food product, in a method for
CC decreasing the time required to dehydrate a composition, to treat a
CC disorder characterised by biocrystals associated with disorders such as
CC gout and kidney stones, to preserve the viability of a molecular biology
CC reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and
CC to protect a plant from damage due to frost or freezing.
XX
SQ Sequence 243 AA;

Query Match 47.3%; Score 655; DB 8; Length 243;
Best Local Similarity 51.9%; Pred. No. 1.8e-49;
Matches 148; Conservative 18; Mismatches 55; Indels 64; Gaps 5;

QY 5 MAKCCMLVFLGLIQLVAGATSWCHHDDLHALRGLAENLSGKGVRLRAWGSAGCCSW 64
DB 1 MAKCWQLLLFLALLPAASAA--SCHPDDLYALRDFAGNLRG--GGVLLRAALPGASCCGW 57

QY 65 EGVGCETASGRVVALRPLKRGLOGIIPSSIGELDLHLYLDLSGNSLVGEVPSQLRLKLS 124
DB 58 EGVGCDGASGCV-----KSFQILLKG 78

QY 125 LTTDSQSLMGSTNMLLHVS--SRTLDEEPNTISGTNNSVSGSNVSGNDNTVVSNN 183
DB 79 LTAAGRSGLGKFTHPLHVKPSQGLTDEHNTITGINTVRSNNVSGNDNTVVSNN 138

QY 184 NHVSGSNNTVVTGSDNTVSGSNHVSGTKHIVTDNNNVSGNDNNVSGSPHTVSGEHTV 243
DB 139 NVVSGSHNTVVFQDGNFISGYHVSGNHHVVTDNKNVSGNDNTVSGSQNTVSGNHQIV 198

QY 244 SGS-----NNTVSGSNHIVSGSNKVVTDG 267
DB 199 SGSHSTVSGNHNNTVSGSNNSVYGNNNIVSGSNHVGVGNKVVTDG 243

RESULT 14
AAAY22472
ID AAY22472 standard; protein; 118 AA.
XX

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```

AC AAY22472;
XX
DT 29-SEP-1999 (first entry)
XX
DE Grass anti-freeze protein sequence.
XX
KW Anti-freeze protein; grass; plant; frozen food product; frost tolerance;
KW frozen confectionery.
XX
OS Lolium perenne.
XX
PN WO9937782-A2.
XX
PD 29-JUL-1999.
XX
PF 23-DEC-1998; 98WO-EP008553.
XX
PR 22-JAN-1998; 98GB-00001408.
XX
PA (UNIL ) UNILEVER NV.
PA (UNIL ) UNILEVER PLC.
XX
XX Jarman CD, Sidebottom CM, Twigg S, Worral D;
XX WPI; 1999-458697/38.
XX N-PSDB; AAX99717.
XX
PT New plant anti-freeze protein useful in frozen food products.
XX
PS Claim 3; Page 36; 39pp; English.
XX
CC This sequence is the plant anti-freeze protein of the invention. The anti-
CC -freeze protein is characterised in that at least 40% of its amino acids
CC are from the group of serine, threonine and asparagine. The anti-freeze
CC protein can be used in frozen food products, especially frozen
CC confectionery. Anti-freeze proteins are especially used in food products,
CC which are heated, e.g. by pasteurisation, blanching or sterilisation
CC prior to freezing. Plants transformed with a nucleic acid sequence
CC encoding the anti-freeze protein have an increased frost tolerance.
CC art anti-freeze proteins have not been applied to commercially available
CC food products, due to high costs and complicated processes for obtaining
CC the protein. Also prior art anti-freeze proteins have tended to
CC destabilise during processing especially during the pasteurisation step.
CC This is overcome by the present anti-freeze protein. The anti-freeze
CC proteins provide an ice particle size following an ice recrystallisation
CC inhibition assay of 15 µm M or less. The anti-freeze protein ingredient
CC means that mixes can be frozen under quiescent conditions, e.g. in a shop
CC or home freezer without the formation of unacceptable ice crystal shapes
CC and hence with a texture different to products normally obtained via
CC quiescent freezing
XX
SQ Sequence 118 AA;

Query Match 38.3%; Score 530; DB 2; Length 118;
Best Local Similarity 85.5%; Pred. No. 7.3e-39;
Matches 100; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 150 DREPNTISGTNNSVSGSNVSGNDNTVVSNNHVSNNNTVVSNDNTVVSNDNTVVSNNHVS 209
DB 1 DEQNPTISGNNTVRSKXVLAGNDNTVSGDNNVSNNNTVVSNDNTVVSNDNTVVSNNHVS 60

QY 210 GTKHIVTDNNNVSGNDNNVSGSFHTVSGEHTVSGSNHIVSGSNHIVSGSNKVVTD 266
DB 61 GTNHIVTDNNNVSGNDNNVSGSFHTVSGEHTVSGSNHIVSGSNHIVSGSNKVVTD 117

RESULT 15
ABB93804
ID ABB93804 standard; protein; 1036 AA.
XX
AC ABB93804;
XX
DT 31-MAY-2002 (first entry)

```


DR N-PSDB; ADM41463.
XX
PT New antifreeze proteins and encoding polynucleotides, useful for
PT modulating cold tolerance in organisms, as food additives, or for
PT treating tumors or disorders associated with the presence of unwanted
PT biocrystals (e.g. gout).
XX
PS Claim 7; SEQ ID NO 19; 71pp; English.
XX
CC The present sequence is that of an antifreeze protein of tall fescue. The
CC invention provides forage grass (perennial ryegrass and tall fescue)
CC antifreeze proteins and the polynucleotides encoding them ADM41458-
CC ADM41483. The polynucleotides were isolated from tissues taken at
CC different times of year (winter and spring) and from different parts of
CC the plants. The polynucleotides can be used to modulate the cold
CC tolerance of an organism, especially plants, mammals, insects, fungi,
CC archaea and bacteria. The method involves incorporating an antifreeze
CC polynucleotide, under the control of a gene promoter sequence, into the
CC genome of the organism, or introducing double-stranded RNA corresponding
CC to the polynucleotide into the cells of the organism, thereby inhibiting
CC expression of an antifreeze polypeptide. The antifreeze protein can be
CC used for the cryopreservation of a cell or tissue, as a food additive of
CC a frozen food product, in a method for decreasing the time required to
CC dehydrate a composition, to treat a disorder characterised by biocrystals
CC associated with disorders such as gout and kidney stones, to preserve the
CC viability of a molecular biology reagent, to destroy unwanted tissue in a
CC patient e.g. tumour tissue, and to protect a plant from damage due to
CC frost or freezing.
XX
SQ Sequence 277 AA;
Query Match 65.6%; Score 908.5; DB 8; Length 277;
Best Local Similarity 67.9%; Pred. No. 8e-72;
Matches 188; Conservative 19; Mismatches 51; Indels 19; Gaps 4;
QY 5 MAKCCWLLVFLGFILOVAGATSWSCCHDDHLALRGLAENLSGKGAVALRAAMSGASCCSW 64
DB 1 MAKCCWLLVFLVLLPAASAT--SCHPDDLRALRGVFNGLG--GGVLLHGAMSGSLCCAW 57
QY 65 EGVGCTASGRVVALRLP-----KRLGGIIPSSIGELDHLRYLSDNS 109
DB 58 EGVGCDGTSGRVTALRLPISLKDCKGLKSLNLANLRLVGTIPSWIGELDHLRYLSDNS 117
QY 110 LVGEVPSLQIRLKSITTSQSLGMSINMLLHV--SSRRTLDEEPTNTSGTNNVSGSN 168
DB 118 LVGKVPNSLQIRLKGATAGSLGMAFANMPLHVKGNNRTLDEQNTTIGTNTVRSND 177
QY 169 NVVSGNDNTVSGNNHVSNNNTVVTGSDNTVGSNNHVSQTKHIVTDNNNVSGNDNN 228
DB 178 NAVSGNDNTVICGNNNTVSGNNNTVSGSDNIVTGSNQVCGTKHITDNNNDVSGNDNN 237
QY 229 VSGSFHTVSGEHTVSGNNNTVSGNNHVSNNHVSNNKVT 265
DB 238 VSGSSHVSHTVSGNNNTVSGNNHVSNNHVSNNKVT 274

RESULT 8
ADM41483
ID ADM41483 standard; protein; 281 AA.
XX
AC ADM41483;
XX
DT 03-JUN-2004 (first entry)
XX
DE Perennial ryegrass antifreeze protein.
XX
KW Antifreeze; perennial ryegrass; cold tolerance; transgenic; plant;
XX antitumor; litholytic; nephrotropic; cytostatic.
XX
OS Lolium perenne.
XX
FH Key Location/Qualifiers
FT Peptide 1..19

FT Region /label= Signal_peptide
FT 10..22 /note= "Conserved lipoprotein membrane attachment site"
FT 53..64 /note= "Conserved Cys-pairs identified N-terminal or
FT leucine-rich repeats of receptor-like kinases"
FT 69..125 /note= "Conserved leucine-rich repeats"
FT 165..279 /note= "7-amino acid sequence repeat region identified in
FT antifreeze proteins"
XX WO2004022700-A2.
XX 18-MAR-2004.
XX 09-SEP-2003; 2003WO-NZ000199.
XX 09-SEP-2002; 2002US-0409557P.
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX (WRIG-) WRIGHTSON SEEDS LTD.
XX Demmer J, Shenk MA, Hall C, Fish SA;
XX WPI: 2004-248453/23.
XX N-PSDB; ADM41470.
XX
XX New antifreeze proteins and encoding polynucleotides, useful for
XX modulating cold tolerance in organisms, as food additives, or for
XX treating tumors or disorders associated with the presence of unwanted
XX biocrystals (e.g. gout).
XX
XX Claim 7; SEQ ID NO 26; 71pp; English.
XX
CC The present sequence is that of an antifreeze protein of perennial
CC ryegrass. The invention provides forage grass (perennial ryegrass and
CC tall fescue) antifreeze proteins and the polynucleotides encoding them
CC ADM41488-ADM41493. The polynucleotides were isolated from tissues taken
CC at different times of year (winter and spring) and from different parts
CC of the plants. The polynucleotides can be used to modulate the cold
CC tolerance of an organism, especially plants, mammals, insects, fungi,
CC archaea and bacteria. The method involves incorporating an antifreeze
CC polynucleotide, under the control of a gene promoter sequence, into the
CC genome of the organism, or introducing double-stranded RNA corresponding
CC to the polynucleotide into the cells of the organism, thereby inhibiting
CC expression of an antifreeze polypeptide. The antifreeze protein can be
CC used for the cryopreservation of a cell or tissue, as a food additive of
CC a frozen food product, in a method for decreasing the time required to
CC dehydrate a composition, to treat a disorder characterised by biocrystals
CC associated with disorders such as gout and kidney stones, to preserve the
CC viability of a molecular biology reagent, to destroy unwanted tissue in a
CC patient e.g. tumour tissue, and to protect a plant from damage due to
CC frost or freezing.
XX
SQ Sequence 281 AA;
Query Match 65.3%; Score 904.5; DB 8; Length 281;
Best Local Similarity 66.5%; Pred. No. 1.8e-71;
Matches 187; Conservative 20; Mismatches 51; Indels 23; Gaps 5;
QY 5 MAKCCWLLVFLGFILOVAGATSWSCCHDDHLALRGLAENLSGKGAVALRAAMSGASCCSW 64
DB 1 MAKCCWLLVFLVLLPAASAT--SCHLDDLRALRGVFNGLG--LNGTWSGSCCDDW 57
QY 65 EGVGCTASGRVVALRLP-----KRLGGIIPSSIGELDHLRYLSDNS 109
DB 58 EGVGCDGTSGRVTALRLPISLKDCKGLKSLNLANLRLVGTIPSWIGELDHLRYLSDNS 117
QY 110 LVGEVPSLQIRLKSITTSQSLGMSINMLLHV--SSRRTLDEEPTNTSGTNNVSG 164
DB 118 LVGKVPNSLQIRLKGATAGSLGMAFANMPLHVKGNNRTLDEQNTTIGTNTVRS 177

Db 241 EHNVTSGSNNVTSGSNHVSGSNKVVTDG 269
|||||
RESULT 3
ADM41481
ID ADM41481 standard; protein; 262 AA.
XX
AC ADM41481;
XX
DT 03-JUN-2004 (first entry)
XX
DE Tall fescue antifreeze protein.
XX
KW Antifreeze; fescue; cold tolerance; transgenic; plant; antigout;
KW litholytic; nephrotropic; cytostatic.
XX
OS Schedonorus arundinaceus.
XX
PH Key Location/Qualifiers
FT Peptide 1..23
FT /label= Signal_peptide
FT Region 57..68
FT /note= "Conserved Cys-pairs identified N-terminal or
FT leucine-rich repeats of receptor-like kinases"
FT Region 73..114
FT /note= "Conserved leucine-rich repeats"
FT Region 147..261
FT /note= "7-amino acid sequence repeat region identified in
FT antifreeze proteins"
XX
PN WO2004022700-A2.
XX
PD 18-MAR-2004.
XX
PF 09-SEP-2003; 2003WO-NZ000199.
XX
PR 09-SEP-2002; 2002US-0409557P.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (WRIG-) WRIGHTSON SEEDS LTD.
XX
PI Demmer J, Shenk MA, Hall C, Fish SA;
XX
DR WPI; 2004-248453/23.
DR N-PSDB; ADM41468.
XX
XX New antifreeze proteins and encoding polynucleotides, useful for
modulating cold tolerance in organisms, as food additives, or for
treating tumors or disorders associated with the presence of unwanted
biocrystals (e.g. gout).
XX
PS Claim 7; SEQ ID NO 24; 71pp; English.
XX
CC The present sequence is that of an antifreeze protein of tall fescue. The
CC encoding cDNA was isolated from a leaf blade cDNA expression library. The
CC invention provides forage grass (perennial ryegrass and tall fescue)
CC antifreeze proteins and the polynucleotides encoding them ADM41458-
CC ADM41483. The polynucleotides were isolated from tissues taken at
CC different times of year (winter and spring) and from different parts of
CC the plants. The polynucleotides can be used to modulate the cold
CC tolerance of an organism, especially plants, mammals, insects, fungi,
CC archaea and bacteria. The method involves incorporating an antifreeze
CC polynucleotide, under the control of a gene promoter sequence, into the
CC genome of the organism, or introducing double-stranded RNA corresponding
CC to the polynucleotide into the cells of the organism, thereby inhibiting
CC expression of an antifreeze polypeptide. The antifreeze protein can be
CC used for the cryopreservation of a cell or tissue, as a food additive of
CC a frozen food product, in a method for decreasing the time required to
CC dehydrate a composition, to treat a disorder characterised by biocrystals
CC associated with disorders such as gout and kidney stones, to preserve the
CC viability of a molecular biology reagent, to destroy unwanted tissue in a
CC patient e.g. tumour tissue, and to protect a plant from damage due to

CC frost or freezing.
XX
SQ Sequence 262 AA;
Query Match 71.7%; Score 992.5; DB 8; Length 262;
Best Local Similarity 75.0%; Pred. No. 2.8e-79;
Matches 198; Conservative 22; Mismatches 39; Indels 5; Gaps 3;
QY 5 MAKCCMLLVFLGLQVAG-ATSWSCHHDDLHALRGLAENLSGKAVRLRAAWSGASCCS 63
Db 1 MAKCLMLLSFAFLLSAAGTATATPCRRDDLRLRGFAENLGGGALSLRAAWSGASCCD 60
QY 64 WEGVGCETASGRVVVALRLPKRGLGGIIPSSIGBLDHLRYLDLGSNLVGEVPKSLQIRLK 123
Db 61 WEGVGCDGASGRVTALWLPKSGLTGPIPSWICQHLRLYLDLGSNALVGEVPKQLQVQLK 120
QY 124 SLTTDSQSLGMSGINMLLVH-SSRRTLDEEPNTISGTNNNSVSGSNVSGNDNTVVSGN 182
Db 121 GLTAAGRS--GFTNMPLHVMNRRLSLDEQNTISGSNNVTVRSGSKNVVAGNDNTVISGD 177
QY 183 NNHVSGSNNVTVTGSDNTVVGSHVVGTKHIVTDNNNVVSGNDNNVSGSFHTVSGEHN 242
Db 178 NNSVSGSNNVTVTGSDNTVVGSHVVGTHIIVTDNNNVVSGNDNNVSGSFHTVSGHNT 237
QY 243 VSGSNNVTGSHNHVSGSNKVVTD 266
Db 238 VSGSNNVTGSHNHVSGSNKVVTD 261
RESULT 4
ADM41480
ID ADM41480 standard; protein; 254 AA.
XX
AC ADM41480;
XX
DT 03-JUN-2004 (first entry)
XX
DE Perennial ryegrass antifreeze protein AFP5.
XX
KW Antifreeze; perennial ryegrass; cold tolerance; transgenic; plant;
KW antigout; litholytic; nephrotropic; cytostatic.
XX
OS Lolium perenne.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT /label= Signal_peptide
FT Region 57..68
FT /note= "Conserved Cys-pairs identified N-terminal or
FT leucine-rich repeats of receptor-like kinases"
FT Region 73..114
FT /note= "Conserved leucine-rich repeats"
FT Region 139..253
FT /note= "7-amino acid sequence repeat region identified in
FT antifreeze proteins"
XX
PN WO2004022700-A2.
XX
PD 18-MAR-2004.
XX
PF 09-SEP-2003; 2003WO-NZ000199.
XX
PR 09-SEP-2002; 2002US-0409557P.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (WRIG-) WRIGHTSON SEEDS LTD.
XX
PI Demmer J, Shenk MA, Hall C, Fish SA;
XX
DR WPI; 2004-248453/23.
DR N-PSDB; ADM41467.
XX
PT New antifreeze proteins and encoding polynucleotides, useful for

PS Claim 7; SEQ ID NO 16; 71pp; English.

XX The present sequence is that of AP2, an antifreeze protein of perennial ryegrass. The encoding cDNA was isolated from a leaf blade cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polynucleotides encoding them ADM41458-ADM41483. The polynucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polynucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze polypeptide. The antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to frost or freezing.

SQ Sequence 267 AA;

Query Match 100.0%; Score 1385; DB 8; Length 267;
Best Local Similarity 100.0%; Pred. No. 5.4e-114;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPEYAKCCMLLVFLGFILOVAGATSWCHHDDLHALRGLAENLSGKGAVALRAAWSGAS 60
DB 1 MPEYAKCCMLLVFLGFILOVAGATSWCHHDDLHALRGLAENLSGKGAVALRAAWSGAS 60

QY 61 CCSWEGVGCETASGRVVALRPLKRGGLGIIIPSSIGELDLRLYLDSGNSLVGEVPSKLIQ 120
DB 61 CCSWEGVGCETASGRVVALRPLKRGGLGIIIPSSIGELDLRLYLDSGNSLVGEVPSKLIQ 120

QY 121 RLKSLTTDSQSLGMSINMLLHVSSRRTLDEEPTISGTTNNVSGSGNNVSGNDNTVVS 180
DB 121 RLKSLTTDSQSLGMSINMLLHVSSRRTLDEEPTISGTTNNVSGSGNNVSGNDNTVVS 180

QY 181 GNNNHVSGSNNTVVTGSDNTVGSNHVSGTKHIVTDNNVSGDNNVSGSFHTVSGSH 240
DB 181 GNNNHVSGSNNTVVTGSDNTVGSNHVSGTKHIVTDNNVSGDNNVSGSFHTVSGSH 240

QY 241 NTVSGSNNTVGSNHVSGSNKVVTDG 267
DB 241 NTVSGSNNTVGSNHVSGSNKVVTDG 267

RESULT 2
ADM41474
ID ADM41474 standard; protein; 269 AA.
AC ADM41474;
XX
XX
DT 03-JUN-2004 (first entry)
XX
XX Tall fescue antifreeze protein.
DE Antifreeze; fescue; cold tolerance; transgenic; plant; antigout;
KW litholytic; nephrotropic; cytostatic.
XX
OS Schedonorus arundinaceus.
XX
XX Key Location/Qualifiers
FH Peptide 1..24
FT /label= signal_peptide
FT 61..72
FT /note= "Conserved Cys pairs identified N-terminal of
FT leucine-rich repeats of receptor-like kinases"
FT 77..118
FT /note= "Conserved leucine-rich repeats"
FT

FT Misc-difference 124
FT /note= "Encoded by TAG"
FT Region 154..268
FT /note= "7-amino acid sequence repeat region identified in
FT antifreeze proteins"

PN WO2004022700-A2.
XX
PD 18-MAR-2004.
XX
XX 09-SEP-2003; 2003WO-NZ000199.
PF
XX 09-SEP-2002; 2002US-0409557P.
PR
XX (GENE-) GENESIS RES & DEV CORP LTD.
PA (WRIG-) WRIGHTSON SEEDS LTD.
XX
XX Demmer J, Shenk MA, Hall C, Fish SA;
XX
XX WPI: 2004-248453/23.
DR N-PSDB; ADM41461.
XX
XX New antifreeze proteins and encoding polynucleotides, useful for
PT modulating cold tolerance in organisms, as food additives, or for
PT treating tumors or disorders associated with the presence of unwanted
PT biocrystals (e.g. gout).
XX
XX Claim 7; SEQ ID NO 17; 71pp; English.

XX The present sequence is that of an antifreeze protein of tall fescue. The
CC encoding cDNA was isolated from a leaf blade cDNA expression library. The
CC invention provides forage grass (perennial ryegrass and tall fescue)
CC antifreeze proteins and the polynucleotides encoding them ADM41458-
CC ADM41483. The polynucleotides were isolated from tissues taken at
CC different times of year (winter and spring) and from different parts of
CC the plants. The polynucleotides can be used to modulate the cold
CC tolerance of an organism, especially plants, mammals, insects, fungi,
CC archaea and bacteria. The method involves incorporating an antifreeze
CC polynucleotide, under the control of a gene promoter sequence, into the
CC genome of the organism, or introducing double-stranded RNA corresponding
CC to the polynucleotide into the cells of the organism, thereby inhibiting
CC expression of an antifreeze polypeptide. The antifreeze protein can be
CC used for the cryopreservation of a cell or tissue, as a food additive of
CC a frozen food product, in a method for decreasing the time required to
CC dehydrate a composition, to treat a disorder characterised by biocrystals
CC associated with disorders such as gout and kidney stones, to preserve the
CC viability of a molecular biology reagent, to destroy unwanted tissue in a
CC patient e.g. tumour tissue, and to protect a plant from damage due to
CC frost or freezing.

XX Sequence 269 AA;

Query Match 93.1%; Score 1290; DB 8; Length 269;
Best Local Similarity 93.3%; Pred. No. 1.4e-105;
Matches 251; Conservative 6; Mismatches 10; Indels 2; Gaps 2;

QY 1 MPEYAKCCMLLVFLGFILOVAGATSWCHHDDLHALRGLAENLSGKGAVALRAAWSGA 59
DB 1 MPEYAKCCMLLVFLGFILOVAGATSWCHHDDLHALRGLAENLSGKGAVALRAAWSGA 60

QY 60 SCCSWEGVGCETASGRVVALRPLKRGGLGIIIPSSIGELDLRLYLDSGNSLVGEVPSKLIQ 119
DB 61 SCCSWEGVGCETASGRVVALRPLKRGGLGIIIPSSIGELDLRLYLDSGNSLVGEVPSKLIQ 120

QY 120 IRLKSLTTDSQSLGMSINMLLHVSSRRTLDEEPTISGTTNNVSGSGNNVSGNDNTV 178
DB 121 IRLKSLTTDSQSLGMSINMLLHVSSRRTLDEEPTISGTTNNVSGSGNNVSGNDNTV 180

QY 179 VSGNNNHVSGSNNTVVTGSDNTVGSNHVSGTKHIVTDNNVSGDNNVSGSFHTVSG 238
DB 181 ISGNNNHVSGSNNTVVTGSDNTVGSNHVSGTKHIVTDNNVSGDNNVSGSFHTVSG 240

QY 239 EHTVSGSNNTVSGSNHIVSGSNKVVTDG 267

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 8, 2005, 02:00:31 ; Search time 167 Seconds
(without alignments)
618.353 Million cell updates/sec

Title: US-10-657-852B-15
Perfect score: 1385
Sequence: 1 MPDYMAKCCMLLVFLGLILQ.....NTVSGSHIVSGNKVVTG 267

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 16Dec04:*
1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1385	100.0	267	8 ADM41473	Adm41473 Perennial
2	1290	93.1	269	8 ADM41474	Adm41474 Tall fesc
3	992.5	71.7	262	8 ADM41481	Adm41481 Tall fesc
4	980.5	70.8	254	8 ADM41480	Adm41480 Perennial
5	973.5	70.3	256	8 ADM41482	Adm41482 Perennial
6	910.5	65.7	277	8 ADM41477	Adm41477 Perennial
7	908.5	65.6	277	8 ADM41476	Adm41476 Tall fesc
8	904.5	65.3	281	8 ADM41483	Adm41483 Perennial
9	901.5	65.1	281	8 ADM41475	Adm41475 Perennial
10	901.5	65.1	285	8 ADM41479	Adm41479 Tall fesc
11	884	63.8	280	8 ADM41478	Adm41478 Perennial
12	668	48.2	243	8 ADM41472	Adm41472 Tall fesc
13	655	47.3	243	8 ADM41471	Adm41471 Perennial
14	530	38.3	118	2 AAY22472	Aay22472 Grass ant
15	258.5	18.7	1036	5 ABB93804	Abb93804 Herbicida
16	204	14.7	1021	8 ADO14158	Ado14158 Carrot ph
17	197.5	14.3	598	3 AAG20654	Aag20654 Arabidops
18	197.5	14.3	599	3 AAG20653	Aag20653 Arabidops
19	197.5	14.3	751	5 ABB93984	Abb93984 Herbicida
20	190.5	13.6	1008	8 ADN72587	Adn72587 Thale cre
21	182	13.1	941	2 AAW68205	Aaw68205 M. catarr
22	181	13.1	653	8 ADJ49621	Adj49621 Oil-assoc
23	177	12.8	892	2 AAW68203	Aaw68203 M. catarr
24	176.5	12.7	735	3 AAG32217	Aag32217 Arabidops
25	176.5	12.7	743	3 AAG32216	Aag32216 Arabidops

ALIGNMENTS

RESULT 1

ADM41473
ID ADM41473 standard; protein; 267 AA.

XX AC ADM41473;

XX DT 03-JUN-2004 (first entry)

XX DE Perennial ryegrass antifreeze protein AFP2.

XX KW Antifreeze; perennial ryegrass; cold tolerance; transgenic; plant;

XX KW antigout; litholytic; nephrotropic; cytosstatic.

XX OS Lolium perenne.

XX Key Location/Qualifiers

FT Peptide 1..23

FT Region 60..71 /label= Signal_peptide

FT /note= "Conserved Cys pairs identified N-terminal of leucine-rich repeats of receptor-like kinases"

FT Region 76..117

FT /note= "Conserved leucine-rich repeats"

FT Region 152..266 /note= "7-amino acid sequence repeat region identified in antifreeze proteins"

WO2004022700-A2.

18-MAR-2004.

09-SEP-2003; 2003WO-NZ000199.

09-SEP-2002; 2002US-0409557P.

(GENE-) GENESIS RES & DEV CORP LTD.
(WRIG-) WRIGHTSON SEEDS LTD.

Demmer J, Shenk MA, Hall C, Fish SA;

WPI: 2004-248453/23.

N-PSDB; ADM41460.

New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted biocrystals (e.g. gout).

```

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 77805
; LENGTH: 3285
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(3285)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_7766C.1
US-10-437-963-77805

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Query Match      8.1%; Score 79.4; DB 19; Length 3285;
Best Local Similarity 63.1%; Pred. No. 2.5e-14;
Matches 157; Conservative 0; Mismatches 86; Indels 6; Gaps 2;

Qy 104 GCAAGCTGCTGTCGTCACACAGACGACCTCCACGCGTTCGAGGGGCTCGCTGAGAAC 163
Db 76 GCTGCGGGCGGCCATGTCACCCGGAAGACCTCTCGGCTCGGGGCATTTGCGGGGAAT 135

Qy 164 CT---AAGCGGCAAGAGGAGCGCTCGCCCTCCGCGCGCATGTCGCGGCGCTCATGCTGC 220
Db 136 CTCTGCGGGTGGGGCGGCGCGGACTCCGCGCGCTCGGGTGAACGCTGCTGC 195

Qy 221 AGCTGGGAAGGTGGGATGCGAAACAGCAAGCGCGCGCTCGTGGCGTTCGCGCTCC 280
Db 196 GCCTGGGACGGGTGCGCTGCGAGCGCGC---CGCCGAGTCACGCGCGTGGCGCTCC 252

Qy 281 AAGCGGCGCTTGGAGGATCATCCATCGATGTTGAGCTTGATCACCCTTCGCTAT 340
Db 253 GGGCGAGGTCTCGAGGGGCCATCCCGCCCTCCCTCGCGCGCTCGCGGCTCCAGGAC 312

Qy 341 TTGGATCTC 349
Db 313 CTCGACCTC 321

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RESULT 15
US-10-260-238-1496
; Sequence 1496, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26

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; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 1496
; LENGTH: 4536
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: N region
; LOCATION: (661)..(661)
; OTHER INFORMATION: n = any nucleotide
US-10-260-238-1496

Query Match      8.1%; Score 79.4; DB 17; Length 4536;
Best Local Similarity 63.1%; Pred. No. 3.1e-14;
Matches 157; Conservative 0; Mismatches 86; Indels 6; Gaps 2;

Qy 104 GCAAGCTGCTGTCGTCACACAGACGACCTCCACGCGTTCGAGGGGCTCGCTGAGAAC 163
Db 76 GCTGCGGGCGGCCATGTCACCCGGAAGACCTCTCGGCTCGGGGCATTTGCGGGGAAT 135

Qy 164 CT---AAGCGGCAAGAGGAGCGCTCGCCCTCCGCGCGCATGTCGCGGCGCTCATGCTGC 220
Db 136 CTCTGCGGGTGGGGCGGCGCGGACTCCGCGCGCTCGGGTGAACGCTGCTGC 195

Qy 221 AGCTGGGAAGGTGGGATGCGAAACAGCAAGCGCGCGCTCGTGGCGTTCGCGCTCC 280
Db 196 GCCTGGGACGGGTGCGCTGCGAGCGCGC---CGCCGAGTCACGCGCGTGGCGCTCC 252

Qy 281 AAGCGGCGCTTGGAGGATCATCCATCGATGTTGAGCTTGATCACCCTTCGCTAT 340
Db 253 GGGCGAGGTCTCGAGGGGCCATCCCGCCCTCCCTCGCGCGCTCGCGGCTCCAGGAC 312

Qy 341 TTGGATCTC 349
Db 313 CTCGACCTC 321

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Job time : 767 secs

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Db 787 AGCTTCCATAAAGTATCTGGAAGTCAAAATACGGTATCTGGGAGCAACAATACCGGTATCC 846
Qy 788 GGGAGCAACCATATCTGATCTGGAGCAAAAGTCGTAAACAGATGGTTAAATTTCTGTA 847
Db 847 GGGAGAAACCATGCTGATCTGGGAGCAAAAGTCGTGACAGAGGTTAAATGATATGT 906
Qy 848 GGTGCA-----GGATTGCTTCCATCTTCCCAAGTTCAGTGTAGCT 887
Db 907 AGTGGATTGTTCCATCTTCCCTAAGGATCTCACGTACTTGACAAAGTTCAGTGTAGCA 966
Qy 888 TACAATCAATAGATGAGACAATCACGTTATGTAATCTCAGG-----ATATGGCATACTT 942
Db 967 CTCATCACTTGGTGGGACAATCCGGTTATGTAACGTCAATGATATAGCATACGTACTT 1026
Qy 943 TTCTTTAAATAAAGCTTCCCTTACATAAATAAAAAA 980
Db 1027 TTCTCTACTTTAAATAAGAAGCTTTCCCTATAAAAAA 1064

RESULT 12
US-10-657-852-2
; Sequence 2, Application US/10657852
; Publication No. US20040146884A1
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jeroen
; APPLICANT: Shenk, Michael Andrew
; APPLICANT: Hall, Claire
; APPLICANT: Fish, Steven A
; TITLE OF INVENTION: Antifreeze proteins isolated from forage
; FILE REFERENCE: 11000.1070U
; CURRENT APPLICATION NUMBER: US/10/657,852
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/409,557
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 959
; TYPE: DNA
; ORGANISM: Festuca arundinacea
US-10-657-852-2

Query Match 27.6%; Score 270.4; DB 22; Length 959;
Best Local Similarity 74.8%; Pred. No. 1.le-77;
Matches 353; Conservative 0; Mismatches 116; Indels 3; Gaps 1;

Qy 383 AGTTTCAGATACGGCTCAAGAGCCTCACACTGACAGCCAGTCACTCGGTATGGTTC 442
Db 292 AGTTTCAGATATTGCTCAAGGGCTCACACCGCTGGCGGTTCACTGGGTAAAGGGTTC 351
Qy 443 ATTAACATGCTATTGTCATGTGAGCAGTAG---AAGAACGCTCGATGAAGAACCAATACA 499
Db 352 ACTAACATGCCATTACATGTGAAGTCTAGCCAAGGAACACTCGACGAAGAACACAATACA 411
Qy 500 ATATCAGGAGCAACAATAGTGTGGATCAGGAGCAACAATGTTGTTTCCGGGAATGAC 559
Db 412 ATAACCTGGGATCAACAATACTGTCAAAATCCGGGAGCAACAATGTTGTTTCTGGGAACGAT 471
Qy 560 AACAGGTGCTATCTGGGAATACACCATGTGCTCGGAGCAACAACACTGTGTAACT 619
Db 472 AACACTGTATATCCGGGAGCAACAACGTCGTGTCGGGAGGCCAACACCGTCGTATTT 531
Qy 620 GGAAGTGACAATCTGTAGTGTGGTACCAACCATGTGCTATCAGGAGCAAAAGCATATTGTT 679
Db 532 GGGGTGACAAATTCCTAAGCGGTAGCAACCATGTGCTATCTGGGAACCAACCATGTGCTG 591
Qy 680 ACTGATAACAATAATGTTGATCCGGGAACGACAATAATGTGTCTGGAAGCTTCCATCT 739
Db 592 ACTGACAAACAAGAATGCCGTATCCGGGGACCAATACTGTATCTGTGGAAGCCAAAATACC 651
Qy 740 GTATCAGGGGAGCACAAATACCGTATCCGGGAGCAACAATACTGTATCCGGGAGCAACCAT 799

Db 652 GTATCCGGGAACCAACCATATCATATCTGGAGCCACAGTACCATATCCGGGAACCACAAT 711
Qy 800 ATCGTATCTGGAGCAACAAGTCGTAAACAGATGGTTAATATTTCTGTAGTG 851
Db 712 ACCGTATCCGGGAGCAACAATTTCTGTATCTGGGAACAACAATATTGTATCTG 763

RESULT 13
US-10-657-852-1
; Sequence 1, Application US/10657852
; Publication No. US20040146884A1
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jeroen
; APPLICANT: Shenk, Michael Andrew
; APPLICANT: Hall, Claire
; APPLICANT: Fish, Steven A
; TITLE OF INVENTION: Antifreeze proteins isolated from forage
; FILE REFERENCE: 11000.1070U
; CURRENT APPLICATION NUMBER: US/10/657,852
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/409,557
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 841
; TYPE: DNA
; ORGANISM: Festuca arundinacea
US-10-657-852-1

Query Match 26.8%; Score 262.2; DB 22; Length 841;
Best Local Similarity 73.5%; Pred. No. 5.3e-75;
Matches 349; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

Qy 380 AAAAGTTTCAGATACGGCTCAAGAGCCTCACACTGACAGCCAGTCACTCGGTATGGGT 439
Db 262 AAGAGCTTCCAGATATTGCTCAAGGGCTCACCGCGTGGCGGTTCACTGGGTAGGCG 321
Qy 440 TCCATTAAATGCTATTGTCATGTGAGCAGTAG---AAGAACGCTCGATGAAGAACCAAT 496
Db 322 TTCCTCACATGCCATTACATGTGAAGCCTAGCAAGGAACACTCGACGAAGACCAAT 381
Qy 497 ACAATATCAGGAGCAACAATAGTGTGGATCAGGAGCAACAATGTTCTTCCGGGAAT 556
Db 382 ACAATAAAGTGGATCAACAATACTGTCTAGATCCGGGAGCAACAATGTTGTTCTGGGAAC 441
Qy 557 GACAACACGGTCTGATCTGGGAATAACAACCATGTGTCTGGGAGCAACAACACTGTGTGA 616
Db 442 GATAACATGTCATATCCGGGAACAACAACGTCGTGTCGGGAGCCACAACCCGTCGTA 501
Qy 617 ACTGGAAGTGACAATCTGTAGTGGTACCAACCATGTGTCATCAGGGAACAAGCATATT 676
Db 502 TTTGGGGTGACAACATTCATAGTGAAGTTACCATGTGTCATCTGGGAACCAACCATGTT 561
Qy 677 GTTACTGATAACAATAATGTTGATCCGGGAACGACAATAATGTGTCTCGAAGCTTCCAT 736
Db 562 GTGACTGACAACAAGAATGCCGTATCCGGGGAGCCAAATCTGTATCTGGAAGCCAAAAT 621
Qy 737 ACTGTATCAGGGAGCAACAATACCGTATCCGGGAGCAACAATACTGTATCTCCGGAGCAAC 796
Db 622 ACCGTATCCGGGAACCAACGATCGTATCTGGGAGCCACAGTACCGTATCCGGGAACCAAC 681
Qy 797 CATATCGTATCTGGGAGCAACAAGTCGTAAACAGATGGTTAATATTTCTGTAGTG 851
Db 682 ATACGGTATCTGGGAGAAACAATTCCTGTATATGGGAACAACAATATTGTATCTG 736

RESULT 14
US-10-637-963-77805
; Sequence 77805, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:


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Db      837  CTGGAGCAACAATACCGTATCGGAGAAACCATGTCGTATCTGGAGCAACAAATCG 896
QY      825  TAACAGATGGTTAATATTCTGTAGGTGCA-----GGATTGCTTCC 864
Db      897  TGACAGAGGTTAATGATATGTTAGTGGATTGTTCCATCTCCCTAAGGGATCTCACGT 956
QY      865  ATCTTCCCAAGTTTCAGTGTAGCTTACAAATCAATAGATGGAGACAATCAGCTTATGTAAT 924
Db      957  ACTTGACAGAGTTTCAGTGTAGCACTCAATCACTTGGTGGGACAATCGGTTATGTAAT 1016
QY      925  TCA--GGATATGCCATATTTTCT 947
Db      1017 TCATGGATATATCATACCTTTCCT 1041

RESULT 9
US-10-657-852-13
; Sequence 13, Application US/10657852
; Publication No. US20040146884A1
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jeroen
; APPLICANT: Shenk, Michael
; APPLICANT: Hall, Claire
; APPLICANT: Fish, Steven A
; TITLE OF INVENTION: Antifreeze proteins isolated from forage
; TITLE OF INVENTION: grasses and methods for their use.
; FILE REFERENCE: 11000.10700
; CURRENT APPLICATION NUMBER: US/10/657,852
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/409,557
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1083
; TYPE: DNA
; ORGANISM: Lolium perenne
US-10-657-852-13

```

```

Query Match      42.8%; Score 419; DB 22; Length 1083;
Best Local Similarity 70.4%; Pred. No. 1.2e-126;
Matches 702; Conservative 0; Mismatches 205; Indels 90; Gaps 7;

QY      33  CCATGCTGAATACATGCGCAAGTGTGATGCTGCTGCTTCTTGGGGTTCATCTTGC 92
Db      45  CCAGAACTTAATCCATGCGGAAATGTTGGTGTGCTCTTCTTGGTGTCTCTTGC 104
QY      93  AGGTGCGAGGACGTCGTGTCGTCACACGACGACCTCCACGCGTTGAGGGCC 152
Db      105  TGGCCATGAGCGGAC-----GTGTCGACCTGGATGACCTCCGCGCGTGGCGGCT 158
QY      153  TCGCTGAGAACCTTAAGCGCAAGAGCGCTCGCTCCGCGCGCATGCTCGGCGCT 212
Db      159  TTGTGCGGAACCTCATATGCG---GGGGTGCCCTTCTCGTGGAACTGCTGCGCTCT 215
QY      213  CATGCTGACGTGGGAAGTGTGGATGCGAAACAGACGCGCGCGCTGCGGCTTGC 272
Db      216  CATGCTGCGATTGGGAAGTGTGGGCTGCGATGGTACAAAGCGCGCGTCAAGCGGCTTGC 275
QY      273  GGCTCC-----CCAAGCGG 287
Db      276  GGCCTCCGATTAAGCTCGAGGACTGCGGTAAGCTCAAGTCGCTCAACCTTGCACGAAA 335
QY      288  GCCTTGGAGGGATCATCCCATCGTCGATTGTTGAGCTTGATCACCTTTCGCTATTGGATC 347
Db      336  GATTGGTGGCAACCATCCCGTGTGGATTGGTGGAGCTTGACCACTGCTACTTGGTTC 395
QY      348  TCTCGGGTAAATCATTTGTTGGGAGGTACC-----AAAAAGTTTGCAGATAC 395
Db      396  TCTCGGATAATTCATTTGTTGGTAGGCAACCAATAGTTTGACAAATAGTTTGCAGATAA 455
QY      396  GGCTCAAGAGCCTCACCACTGACAGCCACTCGGTATGCGTCTTCCATTAAATGCTAT 455

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Db      456  GACTCAAGGSCCTCGCCACCGCTGCTGTTCACTAGGTATGGCTTTCGCTAAATGCCAT 515
QY      456  TGCATGTGA---GCATGAGAAGAACGCTCGATGAAGAACCAATAATATCATAGGACCA 512
Db      516  TGCATGTGAAGGGAACCGAAGAACCCCTCGACGAACAAACAAATACATATCATAGGACCA 575
QY      513  ACAATAGTCTTGGATCAGGAGCAACAATGTTGTTTCCGGGAATGACACACGCTCGTAT 572
Db      576  ACAACACTGTGTAGATCTGGGAACGACAATGCTGTTTCTGGGAACGACACACTGTCTAT 635
QY      573  CTGGGAATAACAACCATGCTCTGGGAGCAACAACACTGTTGTAATCTGGAAGTGACAATA 632
Db      636  GTGGGNAACAACAACACTGCTGTCTGGGAGCAACAACACTTGCATCTGGCAGTGACATA 695
QY      633  CTGTAGTTGGTAGCAACCATGCTGATCAGGAGCAAAAGCATATTTGTACTGTATAACAATA 692
Db      696  TCGTAACTCGGACGAACCATATTTGATGTGGGACCAACATATCATATACTGATAACAACA 755
QY      693  ATGTTGTATCCGGGAACGACAATAATGCTGTCTGGAGCTTCCATATCTATCATAGGGAGC 752
Db      756  ATGACGTATCCGGCAATGATATAATGATATCTGGGAGCTTCCATATCTGTATCGGGAGCC 815
QY      753  ACAATACCGTATCCGGGACCAACAATACTGTAATCTGTAATCTGTAGG-----TGC 852
Db      876  GCAACAAGTCTGTGACAGGAGATGAATGATTTGTGAGGGATGCTTCCATCTTTCTCTAA 935
QY      853  AGGATGCTTCCATCTTCCCAAGTTCAGTGTAGCTTACATCAATAGATGGAGACAATCA 912
Db      936  AGGAGCTCTCACCCCTAGTCCAAAGTTGCGTGCAGCTCACAATCACTTGGTAGGACAATCG 995
QY      913  CGTTATGTAACCTTCA--GGATATGGCATACTTTTCTTT 948
Db      996  AGTTATGTAACCTTCATGGATATAGCATCATCTTCCCT 1032

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```

RESULT 10
US-10-657-852-5
; Sequence 5, Application US/10657852
; Publication No. US20040146884A1
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jeroen
; APPLICANT: Shenk, Michael
; APPLICANT: Hall, Claire
; APPLICANT: Fish, Steven A
; TITLE OF INVENTION: Antifreeze proteins isolated from forage
; TITLE OF INVENTION: grasses and methods for their use.
; FILE REFERENCE: 11000.10700
; CURRENT APPLICATION NUMBER: US/10/657,852
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/409,557
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1084
; TYPE: DNA
; ORGANISM: Festuca arundinacea
US-10-657-852-5

```

```

Query Match      42.6%; Score 417.4; DB 22; Length 1084;
Best Local Similarity 70.3%; Pred. No. 4e-126;
Matches 701; Conservative 0; Mismatches 206; Indels 90; Gaps 7;

QY      33  CCATGCTGAATACATGCGCAAGTGTGATGCTGCTGCTTCTTGGGGTTCATCTTGC 92
Db      46  CCAGAACTTAATCCATGCGGAAATGTTGGTGTGCTGCTCTTCTTGGTGTCTCTTGC 105
QY      93  AGGTGCGAGGAGCAACGTCGTGCTGCTGCCACCAAGACCTCCACGCGTTGAGGGGCC 152

```



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QY 72 TCTTCTGGGTTTCATCTTGCAGGTGGCAGGAG--GCAACGTCGTGGTCTGCGCACCAG 128
DB 104 TCTCCTTCGCGTTCCTTCTGTGTGGTGGCGACGCGCAGCGCATGCGCACCAGCG 163
QY 129 ACGACCTCCACGCGTTCAGGGGCTCGCTGAGAACCTAAGCGGCAAGAGCGCTGCGCC 188
DB 164 ATGACCTTCGCGGCTGCGGGCTCGCTGAGAACCTGCGCGCGCGCGCGCATCAGCC 223
QY 189 TCCGCGCGCATGTCGCGGCTCATGTCGAGCTGGGAGAGTGTGGATGCGGAAACAG 248
DB 224 TCCGCGCGCGTGTGTCAGCGCTCATGTCGAGTGGGAGAGCGTTCGCTGCGCAGGTG 283
QY 249 CAAGCGCGCGTGTGTCAGCGCTTCGCGTCCCAAGCGCGCTTCGAGGATCATCCCAT 308
DB 284 CAGCGCGCGTGTGTCAGCGCTTCGCGTCCCAAGCGCGCTTCGAGGATCATCCCAT 343
QY 309 CQTGATTCGTCAGCTTCGATCACCTTCGCTATTTGGATCTCTCGGGTAATTCATGTTG 368
DB 344 CATGATTCGTCAGCTTCACCACTACGCTACTTCGATCTTCAGGTAATGCTATGTTG 403
QY 369 GGGAGGTACCAAAAGTTTGCAGATACGGCTCAAGAGCTTCACCACTGACAGCCAGTAC 428
DB 404 GCGAGGTACCAAAAGTTTGCAGATACGGCTCAAGAGCTTCACCACTGACAGCCAGTAC 447
QY 429 TCGGTATGGTTCATTAACATGCTATTGCAATGTCG--GCAATGAGAGAGCGCTCGATG 485
DB 448 -----AACATGCTTCATGTCATGTCGTAACAGAGATCCTCGAGC 490
QY 486 AAGAACCAATAAATATCAGGAGCAACAATAGTGTGGATCAGGAGCAACAATGTTG 545
DB 491 AGCAGCCCAATACATTTCTGGAGCAACAATAGTGTGATCCTCGGAGCAACAATGTTG 550
QY 546 TTTCGCGGAATGACAAACGTCGTATCTGGGAATFAACAACATGTCGTGGAGCAACA 605
DB 551 TTGCTGGGAATGACAAACGTCGTATCTGGGAGCAACAATAGTGTGTCGTGGAGCAACA 610
QY 606 ACACCTGTGTAAGTGAAGTGAATGTCGTAGTGTGAGCAACAATGTCGTATCAGGGA 665
DB 611 ACACCTGTGTAAGTGAAGTGAATGTCGTAGTGTGAGCAACAATGTCGTATCAGGGA 670
QY 666 CAAAGCATATGTCATGATAACAATAATGTTGATTCGCGGGAACGACAAATATGTCGTG 725
DB 671 CAAACCATATGTCATGACACACAAATAGTATCAGGGAACGATATGATGATCCG 730
QY 726 GAAGCTTCATATGTCATGAGGAGCAACAATACCGTATCAGGAGCAACAATATGTCAT 785
DB 731 GAGCTTCATATGTCATGAGGAGCAACAATACCGTATCAGGAGCAACAATATGTCAT 790
QY 786 CCGGAGCAACAATATGTCATGAGGAGCAACAATAGTGTGTAACAGATGTTAATATCTG 845
DB 791 CTGGAGCAACAATATGTCATGAGGAGCAACAATAGTGTGTAACAGATGTTAATATCTG 850
QY 846 TAGGTGTCAGGATGTCCTTCATCTT-----CCCAAGTTCAGTGTAGC 886
DB 851 TCAGGCGCATGATGTTTTCACCTTAAGTTCAGTTCAGTTCCTTCAGTTCAGTTCAG 910
QY 887 TTACAATCAATAGATGAGGAGCAACAATACCGTATGTAACCTTCA--GGATATGGCATCTTTC 945
DB 911 TCACAGTCAGTGTGTCGTTCATGCGTATGTAACCTTCACTGATGATATACCATCTTTC 970
QY 946 ---CTTAAATAAAGCTTCCTTTCATATAAATAAATAA 980
DB 971 CTACTATATATAAATAAATTCCTTCATATAAATAAATAA 1008

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RESULT 5
 US-10-657-852-12
 ; Sequence 12, Application US/10657852
 ; Publication No. US20040146894A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Demmer, Jeroen
 ; APPLICANT: Shenk, Michael Andrew

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; APPLICANT: Hall, Claire
; APPLICANT: Fish, Steven A
; TITLE OF INVENTION: Antifreeze proteins isolated from forage
; TITLE OF INVENTION: grasses and methods for their use.
; FILE REFERENCE: 11000.10700
; CURRENT APPLICATION NUMBER: US/10/657,852
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/409,557
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1007
; TYPE: DNA
; ORGANISM: Festuca arundinacea
; US-10-657-852-12

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Query Match 50.3%; Score 492.8; DB 22; Length 1007;
 Best Local Similarity 73.6%; Pred. No. 5.1e-151;
 Matches 739; Conservative 0; Mismatches 197; Indels 68; Gaps 6;

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QY 12 AATCAAGTTCCTTCTTCAATCCATGCTGCAATGCAATGCAATGCAATGCAATGCAATG 71
DB 37 ATTGAATCCATCTATAGCATAGCACTGCTGAATCCATGCGGAATGCTTGATGCTGCTTC 96
QY 72 TCTTCTTGGGTTTCATCTTTCAGAGTGGCAGGAG-----GCAACGTCGTGGTCTGTC 122
DB 97 TCTCTTCGCGTTCCTCTTGTGCGGCGCGCAGCGCGCAGCGCGCAGCGCGCATGCC 156
QY 123 ACCACGACGACCTCCACGCTTGAAGGCGCTCGCTGAGAACTAAAGCGGCAAGAGCGG 182
DB 157 ACCGCGATGACCTTCGCGCGCTGCGGGCTTCGCTGAGAACTGCGGCGCGCGCGCAC 216
QY 183 TCCGCTTCGCGCGCATGCTTCGCGCGCTCATGCTGAGCTGCGGAGGCTGGGATGCG 242
DB 217 TCAGCTTCGCGCGCGCTGCGGCGCTCATGCTGCGATGCGGAGGCTGGGATGCG 276
QY 243 AAACAGCAAGCGCGCGCTGCTGGGTTGCGGCTCCCAAGCGCGCGCTTCGAGGAGTCA 302
DB 277 ACGGTGCGAGCGCGCTGTCAGGCTTGTGGCTCCCAAGGAGCGCGCTTCACGGGCGCA 336
QY 303 TCCCATCTGATGTCAGCTTGCATACCTTCGCTATTTGGATCTTCGCGGTAAATTCAT 362
DB 337 TCCGCTCATGATTTTTCAGCTTCACCACTACGCTACGCTTTCAGGATCTTCAGGTAATG 396
QY 363 TGGTGGGAGGTACCAAAAGTTTGGAGATACGCTCAAGAGCTTCACCACTGACAGCC 422
DB 397 TGGTGGGAGGTACCAAAAGTTTGGAGATACGCTCAAGAGCTTCACCACTGACAGCC 446
QY 423 AGTCACTCGGTATGGGTTCCATTAACATGCTATTGCTATGTA---GCACTAGAAGAACGC 479
DB 447 -----AACATGCCATTCGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 483
QY 480 TCGATGAGAAACCAAAATACAAATATCAGGAGCAACAATAGTGTGGATCAGGAGCAACA 539
DB 484 TCGAGAGCAGCGCAATAACAATTTCTGGAGCAACAATACTGTCAGATCCGCGAGCAAAA 543
QY 540 ATGTTGTTTCCGGAATGACACACGCTGATCTGGGAATAACCAACCATGTCGTCGGA 599
DB 544 ATGTTCTTCTGCGGAATGACACACGCTGATCTGGGAGCAACAATACTGTCGTCGGA 603
QY 600 GCAACAAACATGTTGTAAGTGAACATACTGTAAGTGTGGTGAACCAATGTCGAT 659
DB 604 GCAACAAACATGTTGTAAGTGAACATACTGTAAGTGTGGTGAACCAATGTCGAT 663
QY 660 CAGGAGCAAAAGCATATTTGTAAGTGAACATACTGTAAGTGTGGTGAACCAATGTCGAT 719
DB 664 CAGGAGCAAAAGCATATTTGTAAGTGAACATACTGTAAGTGTGGTGAACCAATGTCGAT 723
QY 720 TGTCTGGAAGCTTCATATGTCATGTCAGGAGCAACAATACCGTATCCGCGGAGCAACA 779
DB 724 TATCCGGAGGCTTCATATGTCATGTCAGGAGCAACAATGTCGTCGCGGAGCAACAATA 783

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Db      1  GCTTCATTCATCAAGGTTCTTGTTCATCCATGCTGAATACATAGGCAAAAGTGTG 60
Qy      61  CATGCTGCTGCTCTTCTTGGGTTTCATCTTGAGTGGGAGGCAAAAGTGTGCTGTG 120
Db      61  CATGCTGCTGCTCTTCTTGGGTTTCATCTTGAGTGGGAGGCAAAAGTGTGCTGTG 120
Qy     121  CCACACGACGACCTCCAGCGCTTGAGGGGCTCTGAGACCTTAAGCGGCAAAAGGAGC 180
Db     121  CCACACGACGACCTCCAGCGCTTGAGGGGCTCTGAGACCTTAAGCGGCAAAAGGAGC 180
Qy     181  CGTCCGCTCCGCGCGCATGCTCGCGGCTCATGCTGCAGCTGGGAGGTTGGGATG 240
Db     181  CGTCCGCTCCGCGCGCATGCTCGCGGCTCATGCTGCAGCTGGGAGGTTGGGATG 240
Qy     241  CGAAACAGCAAGCGCGCTGCTGGGCTTCCCAAGCGCGGCTTGGAGGGAT 300
Db     241  CGAAACAGCAAGCGCGCTGCTGGGCTTCCCAAGCGCGGCTTGGAGGGAT 300
Qy     301  CATCCATCGTGAATGGTGAATCATCACTTCGCTATTTGGATCTCTCGGTAATTC 360
Db     301  CATCCATCGTGAATGGTGAATCATCACTTCGCTATTTGGATCTCTCGGTAATTC 360
Qy     361  ATTGGTTGGGAGGTACCAAAAGTTTGAGATACGGCTCAAGAGCCTCACCACCTGACAG 420
Db     361  ATTGGTTGGGAGGTACCAAAAGTTTGAGATACGGCTCAAGAGCCTCACCACCTGACAG 420
Qy     421  CCAGTCACTCGGTATGGTTCCATTAACTATTTGCATGTGAGCAGTGAAGAACGCT 480
Db     421  CCAGTCACTCGGTATGGTTCCATTAACTATTTGCATGTGAGCAGTGAAGAACGCT 480
Qy     481  CGATGAGAACCAATATCAATATCAGGACCAACATATGTTGATCAGGAGCAACAA 540
Db     481  CGATGAGAACCAATATCAATATCAGGACCAACATATGTTGATCAGGAGCAACAA 540
Qy     541  TGTGTTTCCGGGAATGACAAACGCTCGTATCTGGGAATAACAACATGTGCTGGGAG 600
Db     541  TGTGTTTCCGGGAATGACAAACGCTCGTATCTGGGAATAACAACATGTGCTGGGAG 600
Qy     601  CAACAACTGTGTTAACTGGAAGTGACAAATCTGTAGTTGGTAGCAACCATGTGATC 660
Db     601  CAACAACTGTGTTAACTGGAAGTGACAAATCTGTAGTTGGTAGCAACCATGTGATC 660
Qy     661  AGGACAAAGCATATGTTACTGATAAACAATATGTTGATCCGGGAACGACAATAAGT 720
Db     661  AGGACAAAGCATATGTTACTGATAAACAATATGTTGATCCGGGAACGACAATAAGT 720
Qy     721  GTCTGGAAGCTCCATCTGATCAGGAGGACAAATACCGTATCCGGGAGCAACAATAC 780
Db     721  GTCTGGAAGCTCCATCTGATCAGGAGGACAAATACCGTATCCGGGAGCAACAATAC 780
Qy     781  TGTATCCGGGAGCAACCATATCGTATCTGGGAGCAACAAGTCGTAACAGATGGTTAATA 840
Db     781  TGTATCCGGGAGCAACCATATCGTATCTGGGAGCAACAAGTCGTAACAGATGGTTAATA 840
Qy     841  TTCTGTAGTGCAGGATGCTTCCATCTTCCCAAGTTGAGTGTAGCTTCAATCAATAGA 900
Db     841  TTCTGTAGTGCAGGATGCTTCCATCTTCCCAAGTTGAGTGTAGCTTCAATCAATAGA 900
Qy     901  TGGAGCAATACAGTTATGTAATCTCAGGATATGGCATATCTTCTTTAAATAAGCTT 960
Db     901  TGGAGCAATACAGTTATGTAATCTCAGGATATGGCATATCTTCTTTAAATAAGCTT 960
Qy     961  CCCTTTTACATAAAAAAAA 980
Db     961  CCCTTTTACATAAAAAAAA 980

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RESULT 2
 US-10-657-852-4
 ; Sequence 4, Application US/10657852
 ; Publication No. US20040146884A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Demmer, Jeroen

```

; APPLICANT: Shenk, Michael Andrew
; APPLICANT: Hall, Claire
; APPLICANT: Fish, Steven A
; TITLE OF INVENTION: Antifreeze proteins isolated from forage
; FILE REFERENCE: 11000.1070U
; CURRENT APPLICATION NUMBER: US/10/657,852
; PRIORITY FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/409,557
; PRIORITY FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Festuca arundinacea
; US-10-657-852-4

Query Match      92.3%; Score 904.4; DB 22; Length 996;
Best Local Similarity 96.2%; Pred. No. 8.6e-287;
Matches 949; Conservative 0; Mismatches 31; Indels 6; Gaps 2;

Qy      1  GCTTCATTCATCAAGGTTTCTTGTTCATTCATGCTGAATACATAGGCAAAAGTGTG 60
Db      7  GCTTCATTCATCAAGGTTTCTTGTTCATTCATGCTGAATACATAGGCAAAAGTGTG 66
Qy     61  CATGCTGCTGCTCTTCTTGGGTTTCA---TCTTGAGGTGGCAGGAGCAACGTCGTGTC 117
Db     67  CATGCTGCTGCTCTTCTTGGGCTTCATCTCTTTCAGGTGGCCGAGCAACGTCGTGTC 126
Qy    118  GTGCCACCAACGACGACCTCCACGCTTGAGGGGCTCGCTGAGAACCTTAAGCGGCAAAAG 177
Db    127  GTGCCACCAACGACGACCTCCGCGCATTCGCGGATTCGCGGAGAACCTTAAGCGGCAAAAG 186
Qy    178  AGCGCTCGCCTCCGCGCGCATGCTCGCGGCTCATGCTGACGTGGGAGGTTGGG 237
Db    187  AGCGCTCGCCTCCGCGCGCATGCTCGCGGCTCATGCTGACGTGGGAGGTTGGG 246
Qy    238  ATCGGAAACAGCAAGCGCGCTCGTGGGCTTCCGAGCGGCTCCCAAGCGGCTTGGAGG 297
Db    247  ATCGGAAACAGCAAGCGCGCTCGCGGCTTTCGCGCTCCCAAGCGGCTTGGAGG 306
Qy    298  GATCATCCATCGTCCGATTTGAGTTCGATCACCTTCGCTATTTGGATCTCTCGGGTAA 357
Db    307  GACCATCCATCGTCCGATTTGAGTTCGATCACCTTCGTTGTTGGATCTCTCGGGTAA 366
Qy    358  TTCAATTGTTGGGAGGTACCAAAAGTTTCAGATACGGCTCAAGAGCCTCACCACTGA 417
Db    367  TTCAATTGTTGGGAGGTACCAAAAGTTTCAGATACGGCTCTAGAGCCTCTCCACTGA 426
Qy    418  CAGCCAGTCACTCGGTATGGGTTCCATTAAACATGCTATTTGATGTGAGCAGT---AGAG 474
Db    427  TGGCCAGTCACTCGGTATGGGTTCCATTAAACATGCTATTTGATGTGAGCAGTAAACAGAG 486
Qy    475  AACGCTCGATGAAGAACCAATACAAATACAGGACCAACAATAGTTTGGATCAGGGAG 534
Db    487  AACCTCGATGAAGAACCAATACAAATACAGGACCAACAATAGTTTGGATCAGGGAG 546
Qy    535  CAACAATGTTGTTCCGGGAATGACAAACAGTCGTATCTGGGAATAACAACATGTGTC 594
Db    547  CAACAATGTTGTTCCGGGAATGACAAACAGTCGTATCTGGGAATAACAACATGTGTC 606
Qy    595  TGGGAGCAACAACACTGTTGTAACCTGGAAGTCAACATAGTGTAGTTGGTAGCAACATCT 654
Db    607  TGGGAGCAACAACACTGTTGTAACCTGGAAGTCAACATAGTGTAGTTGGTAGCAACATCT 666
Qy    655  CGTATCAGGACAAAGCATATTTGTTACTGATAAACAATATGTTGATCCGGGAACGACAA 714
Db    667  CGTATCAGGACAAAGCATATTTGTTACTGATAAACAATATGTTGATCCGGGAACGACAA 726
Qy    715  TAATGTGCTGGAAGCTTCCATATCTGATCAGGGAGCAACAATACGTTATCCGGGAGCAA 774
Db    727  TAATGTGCTGGAAGCTTCCATATCTGATCAGGGAGCAACAATACGTTATCTGGGAGCAA 786

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2005, 19:05:46 ; Search time 760 Seconds
(without alignments)

8980.980 Million cell updates/sec

Title: US-10-657-852B-3

Perfect score: 980

Sequence: 1 gcttgattcccaatcaaggt.....ccctttacataaaaaaaaaa 980

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 16886260

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
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- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	980	100.0	980	22	US-10-657-852-3
2	904.4	92.3	996	22	US-10-657-852-4
3	541.6	55.3	1006	22	US-10-657-852-11
4	503.6	51.4	1008	22	US-10-657-852-10
5	492.8	50.3	1007	22	US-10-657-852-12
6	451.2	46.0	1230	22	US-10-657-852-6
7	443.6	45.3	1212	22	US-10-657-852-7
					Sequence 3, Appli
					Sequence 4, Appli
					Sequence 11, Appl
					Sequence 10, Appl
					Sequence 12, Appl
					Sequence 6, Appli
					Sequence 7, Appli

8	421.8	43.0	1246	22	US-10-657-852-9	Sequence 9, Appli
9	419	42.8	1083	22	US-10-657-852-13	Sequence 13, Appl
10	417.4	42.6	1084	22	US-10-657-852-5	Sequence 5, Appli
11	394.4	40.2	1064	22	US-10-657-852-8	Sequence 8, Appli
12	270.4	27.6	959	22	US-10-657-852-2	Sequence 2, Appli
13	262.2	26.8	841	22	US-10-657-852-1	Sequence 1, Appli
14	79.4	8.1	3285	19	US-10-437-963-77805	Sequence 77805, A
15	79.4	8.1	4536	17	US-10-260-238-1496	Sequence 1496, Ap
16	67.2	6.9	495335	22	US-10-737-082-12	Sequence 12, Appl
17	67.2	6.9	495635	22	US-10-765-790-12	Sequence 12, Appl
18	67.2	6.9	705636	22	US-10-737-082-30	Sequence 30, Appl
19	67.2	6.9	705636	22	US-10-765-790-30	Sequence 30, Appl
20	50.8	5.2	2883	19	US-10-437-963-4582	Sequence 4582, Ap
21	50.6	5.2	1912	17	US-10-260-238-568	Sequence 568, App
22	50.6	5.2	2037	19	US-10-437-963-47843	Sequence 47843, A
23	45.4	4.6	2498	13	US-10-027-632-102064	Sequence 102064, A
24	45.4	4.6	2498	13	US-10-027-632-102065	Sequence 102065, A
25	45.4	4.6	2498	13	US-10-027-632-102066	Sequence 102066, A
26	45.4	4.6	2498	17	US-10-027-632-102064	Sequence 102064, A
27	45.4	4.6	2498	17	US-10-027-632-102065	Sequence 102065, A
28	45.4	4.6	2498	17	US-10-027-632-102066	Sequence 102066, A
29	44.8	4.6	1614	19	US-10-437-963-79739	Sequence 79739, A
30	44.8	4.6	3453	14	US-10-101-464A-861	Sequence 861, App
31	44.8	4.6	3453	21	US-10-864-252-861	Sequence 861, App
32	44.6	4.6	2589	19	US-10-437-963-47358	Sequence 47358, A
33	43.8	4.5	235070	13	US-10-087-192-1590	Sequence 1990, Ap
34	43.4	4.4	485	20	US-10-425-115-155868	Sequence 155868, A
35	43.4	4.4	1504	20	US-10-719-993-27	Sequence 27, Appl
36	43.4	4.4	1569	20	US-10-719-993-26	Sequence 26, Appl
37	43.4	4.4	37305	20	US-10-719-993-6767	Sequence 6767, Ap
38	42.8	4.4	2379	19	US-10-437-963-7515	Sequence 7515, Ap
39	42.4	4.3	632	18	US-10-424-599-138064	Sequence 138064, A
40	42.4	4.3	990	20	US-10-425-115-105088	Sequence 105088, A
41	42.4	4.3	2485	18	US-10-425-114-24982	Sequence 24982, A
42	42.2	4.3	2268	19	US-10-437-963-39626	Sequence 39626, A
43	42.2	4.3	2423	20	US-10-425-115-3469	Sequence 3469, Ap
44	41.8	4.3	492	19	US-10-767-701-22961	Sequence 22961, A
45	41.8	4.3	3276	19	US-10-437-963-30048	Sequence 30048, A

ALIGNMENTS

RESULT 1
US-10-657-852-3
; Sequence 3, Application US/10657852
; Publication No. US20040146884A1
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jercoen
; APPLICANT: Shenk, Michael Andrew
; APPLICANT: Hall, Claire
; APPLICANT: Fish, Steven A
; TITLE OF INVENTION: Antifreeze proteins isolated from forage
; FILE REFERENCE: 11000.1070U
; CURRENT APPLICATION NUMBER: US/10/657,852
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/409,557
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 980
; TYPE: DNA
; ORGANISM: Festuca arundinacea
US-10-657-852-3

Query Match 100.0%; Score 980; DB 22; Length 980;
Best Local Similarity 100.0%; Pred. No. 9,9e-312;
Matches 980; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTTGATTCCCAATCAAGGTTCCTTCAATCCATCGCTGAATACATGCAAGTGTG 60
|||||

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QY	544	TGTTCCGGGATGACAAACGTCGTATCTGGGAATAACAACCATGTGTCTGGGAGCAA	603
Db	365	YKMTTKCYCKYRCMWSWCAICYTGYWCYTTKTWGTCTWTKAACTYGTGYSCTKRW	424
QY	604	CAACACTGTTGTAACCTGGA	622
Db	425	YMWTTCTCTWTTWYGTTRA	443

Search completed: October 8, 2005, 20:02:20
Job time : 215 secs

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Db 297 CCTGAGTGTGTTGAATGTTACGCTCTCCCGCTATATTGGGAACCTCTCTCTTTTGGC 356
Qy 337 CTATTGGATCTCTCGGTAATTCATTGTTGGGAGGTACCAAAAAGTTT 387
Db 357 GCATTTAGATCTTTCTTGAATGCTTTTGAAGTGGAGAAATTCAGCAGAGTT 407

RESULT 13
US-10-101-464A-39
; Sequence 39, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; PRIOR FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Pinus radiata
US-10-101-464A-39

Query Match 3.9%; Score 38.2; DB 4; Length 454;
Best Local Similarity 51.5%; Pred. No. 0.077;
Matches 88; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

Qy 217 CTGACGTGGGAAGTGTGGATCGGAACAGCAAGCGCGCTCGTGGCGTTCGGCT 276
Db 237 CTGCTGTGGACGGAATTCGTGAGGCCAAACAGAACAGTGGTTCAATTTCTCT 296
Qy 277 CCCAAGCGCGCCCTTGGAGGATCATCCCATCGTTCGATTCGATGATACCTTCG 336
Db 297 CCTGAGTGTGTTGAATGCTCTCCCGCTATATTGGGAACCTCTCTCTTTTGGC 356
Qy 337 CTATTGGATCTCTCGGTAATTCATTGTTGGGAGGTACCAAAAAGTTT 387
Db 357 GCATTTAGATCTTTCTTGAATGCTTTTGAAGTGGAGAAATTCAGCAGAGTT 407

RESULT 14
US-10-101-464A-421
; Sequence 421, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; PRIOR FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
US-10-101-464A-421

Query Match 3.9%; Score 38.2; DB 4; Length 454;
Best Local Similarity 51.5%; Pred. No. 0.077;
Matches 88; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

Qy 217 CTGACGTGGGAAGTGTGGATCGGAACAGCAAGCGCGCTCGTGGCGTTCGGCT 276
Db 237 CTGCTGTGGACGGAATTCGTGAGGCCAAACAGAACAGTGGTTCAATTTCTCT 296
Qy 277 CCCAAGCGCGCCCTTGGAGGATCATCCCATCGTTCGATTCGATGATACCTTCG 336
Db 297 CCTGAGTGTGTTGAATGCTCTCCCGCTATATTGGGAACCTCTCTCTTTTGGC 356
Qy 337 CTATTGGATCTCTCGGTAATTCATTGTTGGGAGGTACCAAAAAGTTT 387
Db 357 GCATTTAGATCTTTCTTGAATGCTTTTGAAGTGGAGAAATTCAGCAGAGTT 407

RESULT 15
US-09-621-976-15639
; Sequence 15639, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15639
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-15639

Query Match 3.9%; Score 38.2; DB 4; Length 505;
Best Local Similarity 12.3%; Pred. No. 0.082;
Matches 54; Conservative 188; Mismatches 196; Indels 1; Gaps 1;

Qy 184 CCGCTCCGCCCGCATGGTCCGGCGCTCATCTGACGCTGGGAAGGTGGGATGCGA 243
Db 6 SSRYTSSKRYGKYSYSSRWSMKYYAWGRKYGTSGGRCGSGRGMCKWGYRYSY 65
Qy 244 AACAGCAAGCGCGCTCGTGGCGTTCGGCTCCCAAGCGCGCTTGGAGGATCAT 303
Db 66 WGYKWSKSKKWKYSGKMGTSKS-TRKYRYTTSKRTTCKYRWSKWKRMKRWY 124
Qy 304 CCCATCGTGTGATTTGATGATCATCTTCGCTATTTGGATCTCTCGGTAATTCAT 363
Db 125 YYRMKCYSCASYSYRRCRYTGMTRGWYCKRMCKSKSTRYMYTRYWMTGACYGS 184
Qy 364 GTTGGGAGTACCAAAAAGTTTGCAGATACGGCTCAAGAGCTCACCCTGACAGCA 423
Db 185 KMSCKSRSKYSGYKWKYGYKTYMCTSKYKSKMSYKSKMSYKSKMSYKSKMSY 244
Qy 424 GTCATCGTATGGTTCATTAACATGCTATGATGTGAGCAGTAGAAGAACCTCGA 483
Db 245 KKSYYTCKSYTYRTSTSKGWTGKSRWSYTWGCKSKWKRMYSAGAWYAM 304
Qy 484 TGAAGAACCAAAATACATATACAGGACCAACAATAGTGTGGATCAGGAGCAACA 543
Db 305 MSWCMCAWMAWMSRCAWMSKAKKYYMAKSCMYCAKMSKSAKSAKSCGCTTTKY 364
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Db 1783 TCAGGACATGGATTCTCTCTCCACAAATTTGTTCAGACTTGGACTTCAAGACTTTGTATTT 1842
QY 394 ACGGCTCAAG 403
Db 1843 TCCGTTTCATG 1852

RESULT 10
US-10-101-464A-268
; Sequence 268, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 268
; LENGTH: 1107
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-101-464A-268

Query Match 3.9%; Score 38.4; DB 4; Length 1107;
Best Local Similarity 49.6%; Pred. No. 0.12;
Matches 127; Conservative 0; Mismatches 126; Indels 3; Gaps 1;

QY 123 ACCACGACGACTCCACGCGTTGAGGGGCTCGCTGAGAACCTAAGCGGCAAGGAGCGG 182
Db 359 AGCTCACGCCCTCATGGCACTCAAGCGCGCTCGACCCCTCCGCGCGGCTCCTCACCT 418
QY 183 TCCGCTCCGCGCGCATGGTCCGCGCTCATGCTGACGCTGGGAAGGTGGGATCGG 242
Db 419 CGTGTGCGCGCGCGCCCTCGCGCGCGCGCTGCGTTCGAGGGGTGGCGTGG 478
QY 243 AACACGCAAGCGCGCGCTGCGGCTCATGCTGACGCTGGGAAGGTGGGATCGG 302
Db 479 A---CGAGCGCGCGCGCTGGTGAACGCTCGCTGAGGGGAAGGCGCTGAGGGGCGGA 535
QY 303 TCCCATCGTCGATGGTGGAGCTGATCACCTTCGCTATTGATCTCTCGGGTAATTCAT 362
Db 536 TCCGCGCGGAGATCGCGCGGCTCGGGAGCTGACCGGCTGACCTGACCTTCAAGCGCC 595
QY 363 TGGTTGGGGAGGTACC 378
Db 596 TGGGCGCGAGGTGCC 611

RESULT 11
US-10-101-464A-865
; Sequence 865, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
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; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 865
; LENGTH: 2735
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-101-464A-865

Query Match 3.9%; Score 38.4; DB 4; Length 2735;
Best Local Similarity 49.6%; Pred. No. 0.21;
Matches 127; Conservative 0; Mismatches 126; Indels 3; Gaps 1;

QY 123 ACCACGACGACTCCACGCGTTGAGGGGCTCGCTGAGAACCTAAGCGGCAAGGAGCGG 182
Db 343 AGCTCACGCCCTCATGGCACTCAAGCGCGCTCGACCCCTCCGCGCGGCTCCTCACCT 402
QY 183 TCCGCTCCGCGCGCATGGTCCGCGGCTCATGCTGACGCTGGGAAGGTGGGATCGG 242
Db 403 CGTGTGCGCGCGCGCCCTCGCGCGCGCGCTGCGTTCGAGGGGTGGCGTGG 462
QY 243 AACACGCAAGCGCGCGCTGCTGGGCTTCCGAGCTCCCAAGCGCGGCTTGGAGGGATCA 302
Db 463 A---CGAGCGCGCGCGCTGCTGTAACGCTCTCGCTCAGGGGAAGGCGCTGAGGGGCGGA 519
QY 303 TCCCATCGTCGATGGTGGAGCTTGTATCACCTTCGCTATTGATCTCTCGGGTAATTCAT 362
Db 520 TCCGCGCGGAGATCGCGGCTCGGGAGCTGACCGGCTGACCTGACCTTCAAGCGCC 579
QY 363 TGGTTGGGGAGGTACC 378
Db 580 TGGGCGCGAGGTGCC 595

RESULT 12
US-09-228-986-39
; Sequence 39, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-228-986-39

Query Match 3.9%; Score 38.2; DB 3; Length 454;
Best Local Similarity 51.5%; Pred. No. 0.077;
Matches 88; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 217 CTGAGCTTGGGAAGGTGTGGGATGCGAAGCAGACGCGCGCTCGCTTGGCGCT 276
Db 237 CTGCTGTGGAAACGGAATTTCTGCGAGGCCAAACACGAAACGAGTGGTTTCAATTTCTCT 296
QY 277 CCCCAGCGCGGCTTGGAGGATCATCCCATCGTCGATTTGGTGGAGCTTGATCACCCTCG 336
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ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (79)..(735)
FEATURE:
NAME/KEY: gene
LOCATION: (1)..(1028)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (424)..(693)
OTHER INFORMATION: Heat Shock Domain
FEATURE:
NAME/KEY: exon
LOCATION: (1)..(328)
FEATURE:
NAME/KEY: exon
LOCATION: (329)..(1028)
FEATURE:
NAME/KEY: Poly A site
LOCATION: (1028)..(1028)
FEATURE:
NAME/KEY: mRNA
LOCATION: (1)..(1028)
FEATURE:
NAME/KEY: source
LOCATION: (1)..(1028)
OTHER INFORMATION: Zea Mays L., Line B73
FEATURE:
NAME/KEY: transit_peptide
LOCATION: (79)..(213)
FEATURE:
NAME/KEY: 3'UTR
LOCATION: (736)..(1028)
FEATURE:
NAME/KEY: 5'UTR
LOCATION: (1)..(78)
PUBLICATION INFORMATION:
AUTHORS: Lund, Adrian A.
AUTHORS: Blum, Paul H.
AUTHORS: Bhatramakki, Dinakar
AUTHORS: Elthon, Thomas E.
TITLE: Heat-Stress Response of Maize Mitochondria
JOURNAL: Plant Physiol.
VOLUME: 116
PAGES: 1097-1110
DATE: 1998-03-00
US-09-249-180-1

Query Match 4.0%; Score 38.8; DB 3; Length 1028;
Best Local Similarity 52.5%; Pred. No. 0.083;
Matches 85; Conservative 0; Mismatches 77; Indels 0; Gaps 0;
QY 175 AGGAGCGCTCCGGCCCGCGCATGGTCCGGCGCTCATGTGCGAGCTGGGAAGGTGT 234
DB 189 AGTAGCGCGCGCTCCGGGTACACACCGCGCTCCGCTCCGAGCTACGAGGGGC 248
QY 235 GGATCGGAACAGCAGCGCGCGCTCGTGGGTTGGGCTCCCAAGCGCGCTTGG 294
DB 249 CGAGTCGAAGACGATAGCGTCCGCGAGTACGATGGCGGCACGGCGCGGACTACGC 308
QY 295 AGGATCATCCCATCTCGATTGGTGGCTTGATCACCCTCG 336
DB 309 TGTGCCCGCGCTGTCTCAGATATTTCCGTGATCGCTTAG 350

RESULT 8
US-09-434-288-12/c
Sequence 12, Application US/09434288
Patent No. 6303767
GENERAL INFORMATION:
APPLICANT: Betlach C., Melanie
APPLICANT: McDaniel, Robert
TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA

TITLE OF INVENTION: CONSTRUCTS THEREFOR
FILE REFERENCE: 30062-20030.00
CURRENT APPLICATION NUMBER: US/09/434,288
CURRENT FILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: 60/107,093
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 1476
TYPE: DNA
ORGANISM: Streptomyces narbonensis
US-09-434-288-12

Query Match 4.0%; Score 38.8; DB 3; Length 1476;
Best Local Similarity 50.0%; Pred. No. 0.11;
Matches 97; Conservative 0; Mismatches 97; Indels 0; Gaps 0;
QY 85 CATCTTGCGAGGTGGCAGGCAACGTCGTGCTGTCGCCACACGACGACCTCCACGCGTT 144
DB 1281 CCTGCCCGGTGGAGCGGACCCCGCGCTCGGTTCGTCCACGGGACATCCGCGACGC 1222
QY 145 GAGGGGCTCGCTGAGAACCTTAAGCGCAAGAGAGCGCTCCGCTCCGCGCGCATGGTC 204
DB 1221 CGACCTCTCGCCGGGAACTCGCGGGGTGCGACGCGCTCGTCCACTTCGCGCGGAGAG 1162
QY 205 CGGCGCTCATGCTGCAGCTGGGAAGGTGGGATGCCAAACAGCAAGCGCGCGCTCGT 264
DB 1161 CCACGTCGACCGCTCCATCGCGGGGGCTCGGTGTTACCGGGACCAACGTCACGGGCAC 1102
QY 265 GCGGTTGGCGGTCC 278
DB 1101 CGAGACCTGCTCC 1088

RESULT 9
US-10-101-464A-840
Sequence 840, Application US/10101464A
Patent No. 6768041
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 840
LENGTH: 2900
TYPE: DNA
ORGANISM: Pinus radiata
US-10-101-464A-840

Query Match 4.0%; Score 38.8; DB 4; Length 2900;
Best Local Similarity 56.2%; Pred. No. 0.16;
Matches 73; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
QY 274 GCTCCCCAAGCGCGCCCTTGGAGGATCATCCCATCGTCGATGGTGGATGATCACCCT 333
DB 1723 GCTTTCTTACACGCACTTGAAGGTCTGATACAGCTTCAATCAGTGAGCTTCAAAATCT 1782
QY 334 TCGCTATTGGATCTCTCGGGTAATTCTGTTGGGAGGTACCAAAAAGTTTGCAGAT 393

Db 243 TCGCGGGCCCTTCCC 258
 694 TGTTCATCCGGAGACAAATAATGTCTCTGGAAGCTTCCATCTGTATCAGGGAGCA 753
 1203 RRR 1144
 754 CAATACCGTATCCGGAGACAAATACTGTATCCGGAGACCAACCATATCTGTATCTGGAG 813
 1143 RRR 1084
 814 CAACAAAGTCGTACACAGATGTTTATATCTCTAGTGCAGGATGCT 861
 1083 RRR 1036

RESULT 3
 US-10-101-464A-212
 ; Sequence 212, Application US/10101464A
 ; Patent No. 6768041
 ; GENERAL INFORMATION:
 ; APPLICANT: Strabala, Timothy
 ; APPLICANT: Nieuwenhuizen, Nicolaas
 ; APPLICANT: Higgins, Colleen M.
 ; TITLE OF INVENTION: Compositions Isolated from Plant Cells
 ; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
 ; FILE REFERENCE: 11000.1020c2
 ; CURRENT APPLICATION NUMBER: US/10/101,464A
 ; CURRENT FILING DATE: 2002-03-18
 ; PRIOR APPLICATION NUMBER: 09/704,302
 ; PRIOR FILING DATE: 2000-11-01
 ; PRIOR APPLICATION NUMBER: 09/228,986
 ; PRIOR FILING DATE: 1999-01-12
 ; PRIOR APPLICATION NUMBER: 60/162,866
 ; PRIOR FILING DATE: 1999-11-01
 ; PRIOR APPLICATION NUMBER: PCT/US00/00724
 ; PRIOR FILING DATE: 2000-01-11
 ; NUMBER OF SEQ ID NOS: 989
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 212
 ; LENGTH: 408
 ; TYPE: DNA
 ; ORGANISM: Eucalyptus grandis
 US-10-101-464A-212

Query Match 4.2%; Score 41; DB 4; Length 408;
 Best Local Similarity 63.9%; Pred. No. 0.0087;
 Matches 62; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
 291 TTGGAGGGATCATCCCATCGTTCGATTTGGTGAGCTTGATCACCTTCGCTATTTGGATCTCT 350
 114 TCGATGGAAGCATCCCTTTTGGATGGGGAAGATGGAACCTGTTTATTTGGATCTCT 173
 351 CGGTAATTCATTTGGTGGGAGGTACCAAAAGTTT 387
 174 CGAACAACTCTCTTTCTGGGGAGATCCCAAGAGTTT 210

RESULT 4
 US-10-101-464A-221
 ; Sequence 221, Application US/10101464A
 ; Patent No. 6768041
 ; GENERAL INFORMATION:
 ; APPLICANT: Strabala, Timothy
 ; APPLICANT: Nieuwenhuizen, Nicolaas
 ; APPLICANT: Higgins, Colleen M.
 ; TITLE OF INVENTION: Compositions Isolated from Plant Cells
 ; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
 ; FILE REFERENCE: 11000.1020c2
 ; CURRENT APPLICATION NUMBER: US/10/101,464A
 ; CURRENT FILING DATE: 2002-03-18
 ; PRIOR APPLICATION NUMBER: 09/704,302
 ; PRIOR FILING DATE: 2000-11-01
 ; PRIOR APPLICATION NUMBER: 09/228,986
 ; PRIOR FILING DATE: 1999-01-12
 ; PRIOR APPLICATION NUMBER: 60/162,866

Db 243 TCGCGGGCCCTTCCC 258
 454 ATTGCATGTGAGCAGTAGAAGACGCTCGATGAAGAACCAATATACGAGGACCAA 513
 1443 ATTGTGACRR 1384
 514 CAATAGTGTGGATCAGGAGCAACAATGTTTTCGGGAATGACAAACGTCGTATC 573
 1383 RRR 1324
 574 TGGGAATAACCAACATGTCTCGGAGACAAACACTGTTGTAACCTGGAAGTACAAATAC 633
 1323 RRR 1264
 634 TGTAGTTGGTAGCAACCATCTGATCAGGAGCAAAAGCATATTGTTACTGATAACATAA 693
 1263 RRR 1204

US-08-232-463-14/c
 ; Sequence 14, Application US/08232463
 ; Patent No. 5670367
 ; GENERAL INFORMATION:
 ; APPLICANT: DORNER, F.
 ; APPLICANT: SCHEIFLINGER, F.
 ; APPLICANT: FALKNER, F. G.
 ; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 1800 Diagonal Road, Suite 500
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22313-0299
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/232,463
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/935,313
 ; FILING DATE:
 ; APPLICATION NUMBER: EP 91 114 300.6
 ; FILING DATE: 26-AUG-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BENT, Stephen A.
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703)836-9300
 ; TELEFAX: (703)683-4109
 ; TELEX: 899149
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7218 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; CLONE: pTZgpt-F1s
 US-08-232-463-14

Query Match 4.6%; Score 44.8; DB 1; Length 7218;
 Best Local Similarity 4.7%; Pred. No. 0.0033;
 Matches 19; Conservative 216; Mismatches 173; Indels 0; Gaps 0;
 454 ATTGCATGTGAGCAGTAGAAGACGCTCGATGAAGAACCAATATACGAGGACCAA 513
 1443 ATTGTGACRR 1384
 514 CAATAGTGTGGATCAGGAGCAACAATGTTTTCGGGAATGACAAACGTCGTATC 573
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 1323 RRR 1264
 634 TGTAGTTGGTAGCAACCATCTGATCAGGAGCAAAAGCATATTGTTACTGATAACATAA 693
 1263 RRR 1204

US-08-232-463-14/c
 ; Sequence 14, Application US/08232463
 ; Patent No. 5670367
 ; GENERAL INFORMATION:
 ; APPLICANT: DORNER, F.
 ; APPLICANT: SCHEIFLINGER, F.
 ; APPLICANT: FALKNER, F. G.
 ; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 1800 Diagonal Road, Suite 500
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22313-0299
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/232,463
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/935,313
 ; FILING DATE:
 ; APPLICATION NUMBER: EP 91 114 300.6
 ; FILING DATE: 26-AUG-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BENT, Stephen A.
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703)836-9300
 ; TELEFAX: (703)683-4109
 ; TELEX: 899149
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7218 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; CLONE: pTZgpt-F1s
 US-08-232-463-14

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Db 74 GAATGATT 66

Search completed: October 8, 2005, 19:58:39
Job time : 3177 secs

Site 1: EcoRI; Site 2: XhoI; Seeds were germinated and grown at 4 C for 5 weeks. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

ORIGIN

```

Query Match      35.9%; Score 352; DB 2; Length 692;
Best Local Similarity 79.8%; Pred. No. 7.1e-94;
Matches 455; Conservative 0; Mismatches 105; Indels 10; Gaps 3;

QY 275 CTCCTCCACGCGGCTTGGAGGATCATCCCATCGTTCGATTGGTGGAGCTTGATCACCTT 334
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QY 335 CGCTATTGGATCTCTCGGGTAATTCTTGGTGGGAGGTACCAAAAAGTTTGCAGATA 394
Db 66 TGCTACTTGGATCTCTGGATTAATCTTGGTGGGAGGTACCAAGATTT---GATA 122
QY 395 CGGCTCAAGAGCCTCACCACTGACAGCCAGTCACCTCGGTATGGGTTCATTAAACATGTA 454
Db 123 CGGCTCAAGGCTTGTCTCGTCTGTCATTCTACTAGGTATGGTTTTTACTAAACATGCCA 182
QY 455 TTGCATGTGA----GCAGTAGAAGACGCTCGATGAAGAACCAATACAAATATCAGGACC 511
Db 183 TTGTATGTGAAGCGTAATAGAAAGACACTCGAGCAACCAACCAATATCTGGGAGC 242
QY 512 AACATAGTGTGGATCGAGGAGCAACAATGTTTTCGGGAATGACAAACAGCTCTGTA 571
Db 243 AACAACTGTGAGTCTGGGAGCAACAAGTGTGTTTCGGGAATGACAACTGTCTATA 302
QY 572 TCTGGGAATAACAAACATGTGTCGGGAGCAACAACACTGTTGTAACCTGGAAGTGACAAT 631
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Db 363 ACCGTAACCTGGTAGCAACATGTGTCATCTGGGAGCAACAACATATCGTGAACATAAC 422
QY 692 ATGTTGTTATCCGGGAACCAACAATATGTCGGAAGCTTCCATCTGATCTATCAGGGAG 751
Db 423 AATGCGGTATCCGG-----GACAAATATGTCATCCGGAGCTTCCATCCGTTATCCGGAGC 478
QY 752 CACAATACCGTATCCGGGAGCAACAATCTGTATCCGGGAGCAACCATATCGTATCTGGG 811
Db 479 CACAATCTGTATCTGGGAGCAACAACACTGTATCTGGGAGCAACCATGTCGTATCTGGG 538
QY 812 AGCAACAAAGTCGTAACAGATGGTTAAATAT 841
Db 539 AGCAACAAAGTCGTAGGAGATGAATGATTT 568

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RESULT 15

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BE705098/c
LOCUS
DEFINITION
  BE705098 703 bp mRNA linear EST 12-SEP-2000
  Sc02_07e09 A Sc02 AAFEC ECORC cold stressed winter rye seedlings
  Secale cereale cDNA clone Sc02_07e09, mRNA sequence.
ACCESSION
  BE705098
VERSION
  BE705098.1 GI:10093363
KEYWORDS
  EST.
SOURCE
  Secale cereale (rye)
ORGANISM
  Secale cereale
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Poideae; Triticeae; Secale.
  1 (bases 1 to 703)
REFERENCE
  Singh, J.A., Piche, C., Couroux, P., De Moors, A., Harris, L.J.,
  Hattori, J.I., Ouellet, T., Robert, L.S., Sprott, D., and Tinker, N.A.
  Expressed Sequence Tags from Cold-Stressed Winter Rye Seedlings
  Unpublished (2000)

```

COMMENT

Contact: Singh, J.A.
 Eastern Cereal and Oilseed Research Centre
 Agriculture and Agri-food Canada
 KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
 OC6, Canada
 Tel: (613) 759-1662
 Fax: (613) 759-1701
 Email: singhja@agr.gc.ca.

FEATURES

Location/Qualifiers
 1..703
 /organism="Secale cereale"
 /mol_type="mRNA"
 /cultivar="Puma (winter rye)"
 /db_xref="taxon:4550"
 /clone="Sc02_07e09"
 /tissue_type="leaf, crown"
 /dev_stage="seedling three-leaf stage"
 /clone_lib="Sc02_AAFEC_ECORC_cold_stressed_winter_rye_seedlings"
 /note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: Eco RI;
 Site 2: Xho I; Sampled three-leaf seedlings treated for
 one week at 20C, 12 hrs light/day. Library made with
 Stratagene UNIZAP XR Kit/ (not packaged). cDNA is directly
 ligated into SK+/XhoI-EcoRI, then electroporated into
 TOP10 cells (Invitrogen)."

ORIGIN

```

Query Match      35.5%; Score 348.2; DB 2; Length 703;
Best Local Similarity 75.5%; Pred. No. 9.8e-93;
Matches 460; Conservative 0; Mismatches 143; Indels 6; Gaps 2;

QY 236 GGATGCGAAACAGCAAGCGCGGCTCGTGGCTTGGGCTCCCCAAGCGGGCTTGGGA 295
Db 671 GAATCTTGGCAGGCTCGCGGCTGGAGAGCTCAACCTTGCCAAACAGACTGTGC 612
QY 296 GGGATCATCCCATCGTTCGATTGGTGAGCTTCATCACTTCCTTTCGATCTCTCGGGT 355
Db 611 GGCACCATCCCATCGTTCGATTGGCGAGCTTGACCACTTTCGCTACTCTCTCAGAT 552
QY 356 AATTCATTTGGTGGGAGGTACCAAAAAGTTTGAGATACGCTCAAGGCTCACCACCT 415
Db 551 AATTCATTTGATGGCGAGGTGCCAAGAGTTT---GATACGGCTCAAGGGCATCGTCACTC 495
QY 416 GACAGCCAGTCACCTCGGTATGGTTCATTAACATGCTATTGTCATGTGAGCAGTA--GA 472
Db 494 ACTCAATGTTTCACTAGGTATGGATTCTACTAGGTTTCCATTTGATGTGAAGCGTAACCGA 435
QY 473 AGAAGCTCGATGAAGAACCAAAATACAATATCAGGAGCAACAATAGTGTGGATCAGGG 532
Db 434 AGAACACTCGAACCAACCAACCAACAATATCTGGGAGCAACAACACCGTCAGATCTGGC 375
QY 533 AGCAACAATGTTGTTTCGGGAATGACAACACCGTCTGTCGGAATTAACAACCATGTG 592
Db 374 AGCAACAATGTTGTTTCTGGGAACGACCAACACTGTTCATATCCGGGAACAACAACATGTG 315
QY 593 TCTGGGAGCAACAACACTGTTGTTACTGGAAGTGACAATATCTGATGTTGGTAGCAACCAT 652
Db 314 GCTGGAGCAACAACACTGTCTGTAACCGGAGCGACATAACCGTAACCTGGTAGCAACCAT 255
QY 653 GTCGTATCAGGAGCAAAAGCATATTGTTTACTGATAACAATAATGTTGTTATCCGGGAACGAC 712
Db 254 GTCGTATCCGGGAACAACAACATATCGTAACCTGACATAACAATGTAGTATCCGGGAATGAC 195
QY 713 AATAATGTTCTGGAAGCTTCCATCTGTATCAGGAGGAGCAACAATACCGTATCCGGGAGC 772
Db 194 AACAACTGTTATCCGGGGGCTTCCATCTGTATCTGGGAGCCACAATACTGTATCTGGGAGC 135
QY 773 AACATACTGTATCCGGGAGCAACCATATCGTATCTGGGAGCAACAACAGTCCGTAACAGAT 832
Db 134 AACAAACCGTATCTGGGAGCAACCATGTTGTTATCAGGAGGAGCAACAGTCTGTAGGAGAT 75
QY 833 GGTAAATAT 841

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Db      326  TCCGGGAACAACAATGTGGCTGGAGCAACAACACTATCGTAACCGGAACGACAAT 385
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Qy      692  AATGTTGTATCCGGGAACGACAATAATGTCTCTGGAAGCTTCCATACCTGTATCAGGGGAG 751
Db      446  AATGCCGTATCCGGGAATGACAATAATGTATCTGGGAGTTTCCATACCGGTATCCGGAAC 505
Qy      752  CACAATACCGTATCCGGGAGCAACAATACTGTATCTCGGGAGCAACCATATCGTATCTGGG 811
Db      506  CACAATACTGTATCTGGGACCAACAACACTGTATCTGGGAACAACCATGTCGTATCTGGG 565
Qy      812  AGCAACAAGTCTGTACACAGATGTTAAATAT 841
Db      566  AGCAACAAGTCTGTAGGAGATGCATGATTT 595
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RESULT 13
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LOCUS   BJ458121 K. Sato unpublished cDNA library, cv. Akashinriki
DEFINITION
vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone
baak30m05 3', mRNA sequence.
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ACCESSION
VERSION BJ458121 GI:21136659
KEYWORDS
SOURCE   Hordeum vulgare subsp. vulgare
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
```

```
REFERENCE
1 (bases 1 to 689)
Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
Contact: Tadaeu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
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FEATURES
Location/Qualifiers
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/cultivar="Akashinriki"
/sub_species="vulgare"
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/clone="baak30m05"
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Akashinriki vegetative stage leaves"
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Query Match 36.4%; Score 357.2; DB 4; Length 689;
Best Local Similarity 79.1%; Pred. No. 2e-95;
Matches 451; Conservative 0; Mismatches 113; Indels 6; Gaps 2;
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Qy      275  CTCCTCCCAAGCGGGCCCTTGGAGGGATCATCCCATCGTCGATTTGGTGAGCTTGATCACCTT 334
Db      681  CTTTGCAACAACAGACTGGTTGGCACCATCCCGTCATGATTTGGCGAGCTTGACCACTT 622
Qy      335  CGCTATTGGATCTCTCGGGTAATTCATTGGTTGGGAGGATACCAAAAGTTTGCAGATA 394
Db      621  TACTACTTGGATCTTTCCGGATAATTCATTGGTTGGCGAGGTACCCAAAGAGTTT---GATA 565
Qy      395  CGGCTCAAGAGGCTCACCACTGACAGCCAGTCACTCGGTATGGGTTCCATTAAACATGCTA 454
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Db      564  CGGCTCAAGGGCTTCGCCATCGTGTGCTTTCATCAGGTATGATTTTACTAACATGCCCA 505
Qy      455  TTGCATGT---GAGCAGTAGAAGACGCTCGATGAGAACCAAAATACAAATATCAGGAGC 511
Db      504  TTGTATGTGGAGCCTAAACAGAGAATGCTCGACGAACAACCAAAATACAATATCTGGGAGC 445
Qy      512  AACAAATAGTGTGTTGATCAGGGAGCAACAATGTTGTTTCCGGGAATGACAACACGGTCTGTA 571
Db      444  AACACACTGTCTAGATCTGGGAGCACAATGTTGTTCTGGGNAACGACAACACTGTGCTATA 385
Qy      572  TCTGGGAATAACAACCATGTCGTGGAGCAACAACACTGTTGTTAACTGGAAGTGACAAT 631
Db      384  TCCGGGAACAACAACAATGTCGTGGAGCAACAACACTATCTGTAACCGGAACGACAAT 325
Qy      632  ACTGTAGTTGGTAGCAACCATGTCGTATCAGGAGCAAAAGCATATGTTTACTGATACAAAT 691
Db      324  ACCGTAACCTGGTAGCAACCATGTCGTATCTGGGGACAACAACATATCGTAACGACACAAC 265
Qy      692  AATGTTGTATCCGGGAACGACAATAATGTCTGGAAGCTTCCATACCTGTATCAGGGGAG 751
Db      264  AATGCCGTATCCGGGAATGACAATAATGTATCTGGGAGTTTCCATACCGGTATCCGGAAC 205
Qy      752  CACAATACCGTATCCGGGAGCAACAATACTGTATCCGGGAGCAACCATATCGTATCTGGG 811
Db      204  CACAATACTGTATCTGGGACCAACAACACTGTATCTGGGAACAACCATGTCGTATCTGGG 145
Qy      812  AGCAACAAGTCTGTACACAGATGTTAAATAT 841
Db      144  AGCAACAAGTCTGTAGGAGATGCATGATTT 115
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RESULT 14
BF474043
LOCUS   BF474043 D01 H02Z5 Wheat vernalized crown cDNA library Triticum
DEFINITION
aestivum cDNA clone WHE0840_D01_H02, mRNA sequence.
ACCESSION
VERSION BF474043 GI:11543225
KEYWORDS
SOURCE   Triticum aestivum (bread wheat)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
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REFERENCE
1 (bases 1 to 692)
Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D.,
Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J.,
Seaton, C.L. and Tong, J.C.
The structure and function of the expressed portion of the wheat
genomes - Vernalized crown cDNA library
Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.usda.gov
```

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Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
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DEFINITION BJ4622238 K. Sato unpublished cDNA library, cv. Akashinriki
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ACCESSION  BJ4622238
VERSION    BJ4622238.1 GI:21140745
KEYWORDS   EST.
SOURCE     Hordeum vulgare subsp. vulgare
ORGANISM   Hordeum vulgare subsp. vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Poideae; Triticeae; Hordeum.
REFERENCE  1 (bases 1 to 684)
AUTHORS   Sato, K., Saisho, D. and Takeda, K.
TITLE     Barley EST sequencing project in NIG and Okayama Univ
JOURNAL   Unpublished (2002)
COMMENT   Contact: Tadasu Shin-i
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
            Location/Qualifiers
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            Best Local Similarity 78.4%; Pred. No. 1.5e-95;
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QY      265 GCGTTGGCGCTCCCAAGCGGGCTTCGAGGATCATCCCATCGTCGATTGGTGAGCT 324
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QY      325 TGATCACCTTCGCTAFTTGGATCTCTCGGTAATTCATTGGTTGGGAGGTACCAAAAAG 384
Db      619 TGACCACCTTTACTACTTGGATCTTTTCGGATAATTCATTGGTTGGCGAGGTACCAAGAG 560
QY      385 TTTCGAGATACGGCTCAAGAGCTCACCACTGACAGCCAGTCACTCGGTATGGTTCCAT 444
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Db      502 TTACATGCCATTGTATGTGGAGCCTTAACAGAGATGCTTCGACGAACCAACAAATACAT 443
QY      502 ATCAGGAGCAACAATAGTGTGGATCAGGAGCAACAATGTTGTTTCGCGGAATGACAA 561
Db      442 ATCTGGGAGCAACAACACTGTGAGTCTGGGAGCAACAATGTTGTTTCGCGGAACGACAA 383
QY      562 CAGGTCGTATCTGGGAATAACCACTGTGTCTGGGAGCAACAACACTGTGTGTAACGTG 621
Db      382 CACTGTCTATCTCGGGAACAACAACAATGTGGCTGGGAGCAACAACACTATCGTAAACCGG 323
QY      622 AAGTGACATCTAGTGTGGTAGCAACCATGTCGTATCAGGAGCAACAACATATCTTAC 681
Db      322 GAACGACATACCGTAACCTGTGTAGCAACCATGTCGTATCTGGGAGCAACAACATATCGTAA 263
QY      682 TGATACCAATATATGTTATCCGGGAACGACAAATATGTTCTGGAGCTTCATACCTGT 741
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QY      802 CGTATCTGGGAGCAACAAGTCGTAACAGATGGTTAATAT 841
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RESULT 12
BJ450137
LOCUS    BJ450137
DEFINITION
            Hordeum vulgare subsp. vulgare
            BAJ450137 K. Sato unpublished cDNA library, cv. Akashinriki
            vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone
            baak28d17 5', mRNA sequence.
ACCESSION BJ450137
VERSION    BJ450137.1 GI:21128743
KEYWORDS   EST.
SOURCE     Hordeum vulgare subsp. vulgare
ORGANISM   Hordeum vulgare subsp. vulgare
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Poideae; Triticeae; Hordeum.
REFERENCE  1 (bases 1 to 609)
AUTHORS   Sato, K., Saisho, D. and Takeda, K.
TITLE     Barley EST sequencing project in NIG and Okayama Univ
JOURNAL   Unpublished (2002)
COMMENT   Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
            Location/Qualifiers
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            Best Local Similarity 79.1%; Pred. No. 1.9e-95;
            Matches 451; Conservative 0; Mismatches 113; Indels 6; Gaps 2;

QY      275 TTCCCCAAGCGCGCTTGGAGGATCATCCCATCGTCGATTGGTGAGCTTGCATCACCTT 334
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QY      335 CGCTATTGGATCTCTCGGTAATTCATTGGTTGGGAGGTACCAAAAGTTTGCAGATA 394
Db      89  TACTACTTGGATCTTTCGGATAAATTCATTGGTTGGCGAGGTACCAAGAGTTT---GATA 145
QY      395 CGGCTCAAGAGCCTCACCACTGACAGCCAGTCACCTCGGTATGGGTTCCATTAAACATGCTA 454
Db      146 CGGCTCAAGGGCTTCGCCATCGCTCGTTCATCAGGTATGATTTTACTAAACATGCCA 205
QY      455 TTGCAATGT---GAGCAGTAGAAGACGCTCGATGAAGAACCAAAATACAAATATCAGGGACC 511
Db      206 TTGTATGTGGAGCCCTAAACAGAGAATGCTCGAGCAACCAACCAATATATCTGGGAGC 265
QY      512 AACAAATAGTTGGATCAGGAGCAACAATGTTGTTTCGGGAATGACAAACCGTTCGTA 571
Db      266 AACAACTGTGAGTCTGGGAGCAACAATGTTGTTTCGGGAACGACAACTGTGCTA 325
QY      572 TCTGGGAATAACAACCATGTGCTGGGAGCAACAACACTGTTGTTAACTGGAAGTGACAAT 631
```

JOURNAL
COMMENT

Unpublished (2002).
 Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6885
 Email: tshini@genes.nig.ac.jp.

FEATURES
source

ORIGIN

Query Match	36.7%;	Score 359.4;	DB 4;	Length 671;
Best Local Similarity	76.7%;	Pred. No. 4.2e-96;		
Matches 467;	Conservative	0;	Mismatches 136;	Indels 6; Gaps 2;
Qy	236	GGATGCGAAACAGCAAGCGCGCGTTCGTGGCGTTTCGGGTCCCCAAAGCGCGCTTGGGA	295	
Db	53	GCATCCCTTGGCAGGCCTCGCATGTTTGGAGAGCTCAACCTTGCCAAACAAGACTGGTT	112	
Qy	296	GGGATCATCCATCGTTCGATTTGGTGGAGCTTGATCACCTTCGCTATTTGGATCTCTCGGGT	355	
Db	113	GGCACCATCCGTCATGATTTGGCGAGCTTGACCACCTTTACTTACTTTGGATCTTTTCGGAT	172	
Qy	356	AATTCAATTGTTGGGGAGGTACCAAAAGTTTGCAGATACGGCTCAAGAGCCTCACCACT	415	
Db	173	AATTCAATTGTTGGCGAGGTACCCACAGATTTT---GATACGGCTCAAGGGCTTCGCCATC	229	
Qy	416	GACAGCCAGTCACTTCGGTATGGGTTTCATTAACATGCTATTGCAATGT---GAGCAGTAGA	472	
Db	230	GCTGGTGGTTTCATCAGGTATGATTTTCTAAACATGCCATTTGATGTGGAGCCTTAACAGA	289	
Qy	473	AGAACGCTTCGATGAAGAAGACCAATACAAATATCAGGGACCAACAATAGTGTGGATCAGGG	532	
Db	290	AGAAATGCTCAGCAAAACCAACAATACAAATATCTGGAGCAACAACACTGCAGATCTGGG	349	
Qy	533	AGCAACAATGTGTGTTTCCGGGAATGACAAACACGGTCTGTATCTGGGAATAAACAACATGTG	592	
Db	350	AGCAACCAATGTGTTTCTGGGAACGACAAACACTGTCTATATCCGGGAACAACAACATGTG	409	
Qy	593	TCCTGGGAGCAACAACACTGTTGTAACCTGGAAGTGACAATATCTGTAGTTGGTAGCAACCAT	652	
Db	410	GCTGGGAGCAACAACACTATCGTAAACCGGGAAACGACAATACCGTAACTGGTAGCAACCAT	469	
Qy	653	GTGCTATCAGGACAAAGCATATGTTTACTGTATAACAATATGTTGTATCCGGGAACGAC	712	
Db	470	GTGCTATCTGGGACAAACATATCGTAACTTGACAACAACCAATCCGCTATCCGGGAATGAC	529	
Qy	713	AATAAATGTGCTCGAAGCTTCCATCTGTATCAGGGGAGCACAATACCGTATCCGGGAGC	772	
Db	530	AATAAATGTATCTGGAGTTTCCATACCGTATCCGGAAGCCACAATATCTGTATCTGGGACC	589	
Qy	773	AACAATACTGTATCCGGGAGCAACCATATCGTATCTCGGGAGCAACAAGTCGTAAACAGAT	832	
Db	590	AACAACACTGTATCTGGGAACAACCATGTGCTATCTCGGGAGCAACAAGTCGTAGGAGAT	649	
Qy	833	GGTTAATAT	841	
Db	650	GCATGATTT	658	

RESULT 11
BJ462238/C

ORIGIN		Query Match		Best Local Similarity		Matches		Conservative		0;		Mismatches		133;		Indels		6;		Gaps		2	
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Qy	241	CGAAACAGC	CGCGCGCTCGTGGCGTCCCGGCTCCCAAGCGCGGCTTGGAGGAT	300	37.0%	Score	362.2;	DB	4;	Length	632;												
Db	1	CGAGCGAGG	CGCTCGATCGTTGGAGGAGCTCAACCTTGCCACACAGACTGGTTGGCAC	60	77.1%	Pred. No.	6e-97;																
Qy	301	CATCCCATCGT	CGAATGGTGAGCTTGATCACCTTCGCTATTATTGGATCTCTCGGTAATTC	360																			
Db	61	CATCCCGTCA	TGGATTGGCGAGCTTGACCACTTTACTACTTTGGATCTTTCCGATAATTC	120																			
Qy	361	ATTGGTTGGG	GAGGTACCAAAAAGTTTGCAGATACGGCTCAAGAGCCTCACCATCTGCAG	420																			
Db	121	ATTGGTTGG	CGAGGTACCAAGAGTTT---GATACGGCTCAAGGCTTCGCCATCGCTGG	177																			
Qy	421	CCAGTCACT	CGGTATGGGTTCCATTAAATGCTATTGTCATGT---GAGCAGTAGAAGAAC	477																			
Db	178	TCGTTTCAT	CAGGTATGATTTTATTCTAAATGCCATTGTTATGTGGAGCCTTAACAGAGAAT	237																			
Qy	478	GCTCGATC	AGAACCAATAAATATCAGGACCAACAATAATGTTGATCAGGGAGCAA	537																			
Db	238	GCTCGAGCA	ACCAATAAATATCTGGGAGCAACAACACTGTTCAGATCTGGAGGAC	297																			
Qy	538	CAATGTTGTTT	CCGGGAATGACAAACGGTCTGTTATCTGGGAATAACAACCATGTCTCTGG	597																			
Db	298	CAATGTTGTTT	CTGGGAACGACACATGTCATATCCGGGAACAACAATGTGGCTGG	357																			
Qy	598	GAGCAACAAC	ACTGTTGTAATCTGGAAGTGACAAATCTGTAGTTGGTAGCAACCATGTGCT	657																			
Db	358	GAGCAACAAC	ACTATCGTTAAACCGGGAAACGACAAATACCGTAACTGGTAGCAACCATGTGCT	417																			
Qy	658	ATCAGGACA	CAAGCATATTTGTTACTGATAACAATAATGTTGTATCCGGGAACGACAAATA	717																			
Db	418	ATCTGGGG	CAAAACATATCGTAACTGCAACAACAATGCCGTATCCGGGAATGCAATAA	477																			
Qy	718	TGTCCTCGG	AGCTTCCATACCTGTATCAGGGGAGCACAAATACCGTATCCGGGAGCAACA	777																			
Db	478	TGTAATCTG	GGAGTTTCCATACCGTATCCGGGAAGCACAAATGTAATCTGGGAACCAACA	537																			
Qy	778	TACTGTATC	CGGGAGCAACCATATCGTATCTGGGAGCAACAAGTCGTAAACAGATGGTTA	837																			
Db	538	CACGTGTAT	CGGGAACCAACCATGCTATCTGGGAGCAACAAGTCGTAGGAGATGCATG	597																			
Qy	838	ATATTCT	844																				
Db	598	ATTTTGT	604																				

RESULT	10
BJ454271	
LOCUS	BJ454271 K. Sato unpublished cDNA library, cv. Akashinriki
DEFINITION	vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone baak46n01 5', mRNA sequence.
ACCESSION	BJ454271
VERSION	BJ454271.1 GI:21132845
KEYWORDS	EST.
SOURCE	Hordeum vulgare subsp. vulgare
ORGANISM	Hordeum vulgare subsp. vulgare
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum. 1 (bases 1 to 671)
REFERENCE	Sato,K., Saisho,D. and Takeda,K.
AUTHORS	Barley EST sequencing project in NIG and Okavama Univ
TITLE	

QY 812 AGCAACAAAGTCGTAAACAGATGGTTAAATAT-----TCTGTAGGTGACGGA 856
 Db 146 AGCAACAAAGTCGTAGGAGATGCATGTTGTAAGTGGAGTCTCATCTTCGTGACGGA 87
 QY 857 TTGCTTCATCTTCCCAAGTTCAGTGTAGCTTACAAATAGATGGAGACAATCACGTT 916
 Db 86 GCTCACCTTGTGTCCGAGTTCGGTGTAGCTCACAAATCACTTGTGTGGGGCCAATCGTGT 27
 QY 917 ATGTAACT 924
 Db 26 ATGAACCT 19

RESULT 8
 BE490074
 LOCUS
 DEFINITION
 Triticum aestivum cDNA clone WHE0365_G07_N13, mRNA sequence.

ACCESSION
 BE490074
 SOURCE
 EST.
 Triticum aestivum (bread wheat)

ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.

REFERENCE
 AUTHORS
 Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D.,
 Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J.,
 Seaton, C.L. and Tong, J.C.
 The structure and function of the expressed portion of the wheat
 genomes - Cold-stressed seedling cDNA library
 Unpublished (2000)

JOURNAL
 COMMENT
 Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA

Tel: 510595773
 Fax: 510595818
 Email: oanderson@pw.usda.gov

Sequence have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20

Seq primer: Stratagene SK primer.

FEATURES
 source

1..588
 Location/Qualifiers
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="WHE0365_G07_N13"
 /tissue_type="Seedling"
 /dev_stage="Five-day old seedling"
 /lab_host="E. coli SOLR"
 /clone_lib="Wheat cold-stressed seedling cDNA library"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
 Site 1: EcoRI; Site 2: XhoI; Seeds were
 surface-sterilized, germinated and grown aseptically in
 the dark at room temperature on filter paper with water,
 nystatin and cefotaxime in covered crystallization
 dishes. Five-day old seedlings were transferred to 5 C
 cold room and kept for 48 hr. The tissue, total RNA, and
 poly(A) RNA were prepared, a cDNA library was made, and
 the cDNA clones were in vivo excised to give phagescript
 phagemids in the T7 Close Lab (Choi, Close, Fenton) at
 the University of California, Riverside. Plasmid DNA
 preparations and DNA sequencing were performed in the OD
 Anderson lab (all other authors)."

ORIGIN

Query Match 37.0%; Score 362.4; DB 2; Length 588;
 Best Local Similarity 79.5%; Pred. No. 5.2e-97;
 Matches 455; Conservative 0; Mismatches 111; Indels 6; Gaps 2;

QY 257 CGCGTCGTGGCGTTTCGGCTCCCAAGCGCGCGCTTGGAGGATCATCCCATCGTCGATT 316
 Db 20 CGGCTAGAGGAGCTCAACCTTTGCCAAACAACTGGTCGGTACCATCCCATCGTGGATT 79
 QY 317 GGTGAGCTTGATCACTTCGCTATTCGATCTCTCGGTAATTCATTCTGTTGGGAGGTA 376
 Db 80 GCGAGCTTGATCACTTCGCTATTCGATCTCTCGGTAATTCATTCTGTTGGGAGGTA 139
 QY 377 CCAAAAAGTTTGCAGATACGGCTCAAGAGCGCTCACCACTGCACAGCCAGTCACTCGGTATG 436
 Db 140 CCAAGAGTTT--GATACGGCTCAAGGCTCTCGTCATCGTTGGTCGTTCACTAGGTATG 196
 QY 437 GGTTCATTAACATGCTATTCGATGTGA--GAGTAGAAGAAACCTCGATGAAGAACCA 493
 Db 197 GTTTTACGAACATGCCATTGTATGTGAAGCGTATAGAGAACAACACTCGACGAACAACCA 256
 QY 494 AATCAATATCAGGAGCAACAATAGTCTTCGATCAGGAGCAACAATGTTGTTCCGG 553
 Db 257 AATCAATATCTGGGAGCAACAACACTGTCAATCTGGAAGCACCACGTTGTTTCTGG 316
 QY 554 AATGACAAACCGTCTGTATCTGGGAATAAACCACTGTCTGGGAGCAACAACACTGTT 613
 Db 317 AATGACAAACCTGTCTATTCGGGATTAACCAATGTGGCTGTAGCAACAACACTGTC 376
 QY 614 GTAACTGGAAGTGACAATCTAGTGTAGTGTAGCAACCACTGTCTATCAGGAGCAACAAGCAT 673
 Db 377 GTAACTGGAAGTGACAATCTAGTGTAGTGTAGCAACCACTGTCTATCTGGGAGCAACAACAT 436
 QY 674 ATTGTTACTGATAACAATTAATGTTGTATCCGGAGCAACAATGTTCTCTGGAAGCTTC 733
 Db 437 ATCGTGACTGACAATAACAATGCCGTATCCGGGAATGACAATAATGTTATCTGGGAGCTTC 496
 QY 734 CATATCTGTATCAGGGAGCAACAATACCTGTATCCGGGAGCAACAATCTGTATCTCCGGAGC 793
 Db 497 CATACCGTATCCGGAGCAACAATCTGTATCTGGGAGCAACAACACTGTATCCGGAAGC 556
 QY 794 AACCATATCGTATCTGGGAGCAACAAGTCGT 825
 Db 557 AACCATGTCTGTATCTGGGAGCAACAAGTCGT 588

RESULT 9
 BE453251
 LOCUS

DEFINITION

BJ453251 K. Sato unpublished cDNA library, cv. Akashinriki
 vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone

baak42804 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Poideae; Triticeae; Hordeum.
 1 (bases 1 to 632)

Sato, K., Saisho, D. and Takeda, K.
 Barley EST sequencing project in NIG and Okayama Univ

Unpublished (2002)
 Contact: Tadao Shin-i

Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.

Location/Qualifiers
 1..632

organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"

/cultivar="Akashinriki"

/sub_species="vulgare"

/db_xref="taxon:112509"

SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 686)

AUTHORS Sato, K., Saisho, D. and Takeda, K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES

source

1..686
Location/Qualifiers
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Akashinriki"
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/db_xref="taxon:112509"
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/dev_stage="vegetative stage"
/clone_lib="K. Sato unpublished cDNA library, cv.
Akashinriki vegetative stage leaves"

ORIGIN

Query Match 37.8%; Score 370.2; DB 4; Length 686;
Best Local Similarity 75.6%; Pred. No. 2.5e-99;
Matches 507; Conservative 0; Mismatches 143; Indels 21; Gaps 3;

QY 275 CTCCCCAAGCGCGCTTGGAGGATCATCCCATCGTGGTGGAGCTTGATCACCTT 334

DB 684 TTGTCACAAACAGACTGGTTGGCACCATCCCGTCATGGATTGGCGAGTTGACCACTT 625

QY 335 CGCTATTGGATCTCTCGGGTAATTCATTGGTTGGGGAGGTACCAAAAAGTTTGAGATA 394

DB 624 TACTACTTGGATCTTTCCGGAATAATTCATTGGTTGGCGAGGTACCCAAAGAGTTT---GATA 568

QY 395 CGGCTCAAGAGCTCACCACCTGACAGCCAGTCACTCGGTATGGTTCCATTAAACATGCTA 454

DB 567 CGGCTCAAGGGCTTCCCATCGTGTCTGTTTCATCAGGTATGATTTTACTACATGCCA 508

QY 455 TTGTCATGT---GAGCAGTAGAAGAACGCTCGATGAAGAACCAAAATACATATCAGGGACC 511

DB 507 TTGTTATGGAGCCTAACAGAGAATGCTCGACGAACAAACCAATAATATCTGGGAGC 448

QY 512 AACATATGTTGGATCAGGGAGCAACAATGTTGTTCCGGGAATGACAAACAGGTCGTA 571

DB 447 AACAACTGTGATCTGGGAGCACCAATGTTGTTCTGGGAACGACAACTGTGTCATA 388

QY 572 TCTGGGAATAACAACATGTTCTGGAGCAACAACACTGTTCTTAACCTGGAAGTGACAT 631

DB 387 TCCGGGAACAACAACATGTGGCTGGGAGCAACAACACTATCGTAACCGGGAACGACAAT 328

QY 632 ACTGTAGTTGGTAGCAACCATGTGCTATCAGGAGCAAAAGCATATTGTTACTGATACAAAT 691

DB 327 ACGTAACTGGTAGCAACCATGTGCTATCTGGGACAAACATATCGTAACCTGACAAAC 268

QY 692 AATGTTGTATCCGGGAACGACAATAATGTGTCTGGAAGCTTCCATATCTGATCAGGGAG 751

DB 267 AATGCCGTATCCGGGAATGACAATAATGTATCTGGGAGTTTCCATACCGGTATCCGGAAC 208

QY 752 CACATACCGTATCCGGGAGCAACATAGTATCGGGAGCAACCATATCGTATCTGTTGGG 811

DB 207 CACAATCTGTATCTGGGAGCAACAACACTGTATCTGGGAACAACCATGTCGTATCTGGG 148

QY 812 AGCAACAAAGTCGTACAGATGGTTAATAT-----TCTGTAGTGTGAGGA 856

DB 147 AGCAACAAAGTCGTAGGAGATGCATGATTTGTAAGTGGAGTGTCCATCTTCCGTGACGA 88

QY 857 TTGCTTTCATCTTCCCAAGTTCAGTGTAGCTTACAATAGATGAGACATACGTT 916
DB 87 GCTCACCTTGTGTCGAGTTCGGTGTAGCTCACATCACTTGGTGGGCCAATCGTGT 28
QY 917 ATGTAACCTCA 927
DB 27 ATGTAACCTCA 17

RESULT 4

BJ461803/c

LOCUS

DEFINITION

vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone

baak46n01 3', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Hordeum vulgare subsp. vulgare

Hordeum vulgare subsp. vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Poideae; Triticeae; Hordeum.

REFERENCE

1 (bases 1 to 699)

AUTHORS

Sato, K., Saisho, D. and Takeda, K.

TITLE Barley EST sequencing project in NIG and Okayama Univ

JOURNAL Unpublished (2002)

COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES

Location/Qualifiers

1..699

/organism="Hordeum vulgare subsp. vulgare"

/mol_type="mRNA"

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/clone_lib="K. Sato unpublished cDNA library, cv.
Akashinriki vegetative stage leaves"

ORIGIN

Query Match 37.8%; Score 370.2; DB 4; Length 699;

Best Local Similarity 75.6%; Pred. No. 2.5e-99;

Matches 507; Conservative 0; Mismatches 143; Indels 21; Gaps 3;

QY 275 CTCCCCAAGCGCGCTTGGAGGATCATCCCATCGTGGTGGAGCTTGATCACCTT 334

DB 686 CTTGCCAAACAGACTGGTTGGCACCATCCCGTCATGATGGCGAGTTGACCACTT 627

QY 335 CGCTATTGGATCTCTCGGGTAATTCATTGGTTGGGGAGGTACCAAAAAGTTTGAGATA 394

DB 626 TACTACTTGGATCTTTCCGGAATAATTCATTGGTTGGCGAGGTACCCAAAGAGTTT---GATA 570

QY 395 CGGCTCAAGAGCTCACCACCTGACAGCCAGTCACTCGGTATGGTTCATTAACATGCTA 454

DB 569 CGGCTCAAGGGTTCCCATCGTGTGCTTCATCAGGTATGATTTTACTAACATGCCA 510

QY 455 TTGTCATGT---GAGCAGTAGAAGAACGCTCGATGAAGAACCAAAATACATATCAGGGACC 511

DB 509 TTGTTATGGAGCCTTAACAGAAAGATGCTTCGAGAACAAACAAATATCTGGGAGC 450

QY 512 AACAAATAGTTGGATCAGGGAGCAACAATGTTGTTTCCGGGAATGACAAACGCGTCTGA 571

DB 449 AACAACTGTGATCTGGGAGCACCAATGTTGTTTCTGGGAACGACAACTGTGTCATA 390

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QY 293 GGAGGATCATCCATCGTCGATGGTGAGCTTGATCACCTTCGCTATTTGGATCTCTCG 352
DB 87 GTTGGACCATCCCGTCATGGATTGGCGAGCTTGACACCTTTACTTGTGATCTTTTCG 146
QY 353 GGTAAATTCATTTGGTGGGAGGTACCAAAAGTTTTCGATACGGCTCAAGAGCCTCAC 412
DB 147 GATAATTCATTTGGTGGGAGGTACCAAGAGTTT--GATACGGCTCAAGGGCTTCGCC 203
QY 413 ACTGACAGCAGTCACTCGTATGGTTCCTATTAACATGCTATTTGATGT---GAGCAGT 469
DB 204 ATCGTGTGTCATCGATGATGATTTTACTAATGCTATTTGATGAGGCTTAAC 263
QY 470 AGAAGACCTCGATCAAGAACCAATAAATATCAGGGACCAACAATAGTGTTCGATCA 529
DB 264 AGAAGAATGCTCGAGAACCAACAATAATATCTGGGAGCAACAACATCTGATGATCT 323
QY 530 GGGAGCAACAATGTTGTTTCCGGGATGACACACGGTCTGATCTCGGGAATAAACCAAT 589
DB 324 GGGAGCAACAATGTTGTTTCCGGGAGCAACAACATCTGATCTCGGGAACAACAAT 383
QY 590 GTGCTGGGAGCAACAACATCTGTTGTAATCGGAAGTGACAATCTGTTAGTGGTAGCAAC 649
DB 384 GTGGCTGGGAGCAACAACATCTGTAACCGGGAACGACAATACCGTAACCTGTTAGCAAC 443
QY 650 CATGTCGTATCAGGACAAAGCATATTTGTTACTGATAACAATAATGTTGTTATCCGGAAC 709
DB 444 CATGTCGTATCTGGGACAAACATATCGTAACCTGACAAACAATGCGGTATCCGGGAAT 503
QY 710 GACAATAATGTCGTGGAAGTTCATATCTGATCAGGGGAGCAACAATACCGTATCCGGG 769
DB 504 GACAATAATGTCGTGGAAGTTCATATCTGATCAGGGGAGCAACAATACCGTATCTGGG 563
QY 770 AGCAACAATCTGTATCCGGGAGCAACAATCTGATCTGGGAGCAACAATGTTAGTAAACA 829
DB 564 ACCAACAACATCTGTATCTGGGAGCAACAATCTGATCTGGGAGCAACAATGTTAGTAA 623
QY 830 GATGTTATAT-----TCTGTAGTGCAGGATGCTTCCATCTTCCCA 874
DB 624 GATGATGATTTGTAAGTGGAGTGTCCATCTTCCGTGAGGAGCTCACCTTGTGTCGA 683
QY 875 GTTCACTGTAGTTCATAATCAATAGATGGAGCAATCACTGTTATGTAACCTCA 927
DB 684 GTTCGTGTAGTTCACATCACTGTGTGGGGCAATCGTGTATGTAACCTCA 736

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RESULT 2

BJ458554/c
LOCUS
DEFINITION
746 bp mRNA linear EST 23-MAY-2002
vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone
baak32hi6 3', mRNA sequence.

ACCESSION

BJ458554

VERSION

BJ458554.1

KEYWORDS

EST.

SOURCE

Hordeum vulgare subsp. vulgare

ORGANISM

Hordeum vulgare subsp. vulgare

REFERENCE

Sato, K., Saisho, D. and Takeda, K.

Barley EST sequencing project in NIG and Okayama Univ

Unpublished (2002)

Contact: Tadasu Shin-i

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp.

FEATURES

Location/Qualifiers

1..746

/organism="Hordeum vulgare subsp. vulgare"

/mol_type="mRNA"
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/clone_lib="K. Sato unpublished cDNA library, cv.
Akashinriki vegetative stage leaves"

ORIGIN

Query Match 38.0%; Score 372.4; DB 4; Length 746;
Best Local Similarity 73.7%; Pred. No. 5.5e-100;
Matches 523; Conservative 0; Mismatches 166; Indels 21; Gaps 3;
QY 236 GGATCGGAAAACAGAACGCGCGCTCGTGGGTGGCGCTCCCAAGCGGCGCTTGA 295
DB 717 GCATCTTTGGGAGGCTCGCATGTTGGAGAGCTCAACCTTGGCAACAACAGACTGGTT 658
QY 296 GGGATCATCCCATCGTCGATTTGGTGAGCTTCATACACCTTCGCTATTTGGATCTCTCGGT 355
DB 657 GGCACCATCCCGTCATGATTTGGGAGCTTGACACCTTTACTTCTGATCTTTCCGAT 598
QY 356 AATTCATTTGGTGGGAGGTACCAAAAAGTTTTCGAGATACGCTCAAGAGCCTCACCACT 415
DB 597 AATTCATTTGGTGGGAGGTACCAAGAGTTT---GATACGGCTCAAGGGCTTCGCCATC 541
QY 416 GACAGCCAGTCACTCGGTATGCGTTCATTAACATGCTATTTGCATGT---GAGCAGTAGA 472
DB 540 GCTGCTGCTTCATCAGGTATGATTTTACTAATGATGCTTGTATGTGGAGCCTAACAGA 481
QY 473 AGACGCTCGATGAGAACCAATATCAATATCAGGGAGCAACAATAGTGTGGATCAGGG 532
DB 480 AGAATGCTCGAGCAACAACCAATAACAATATCTGGGAGCAACAACACTGTGATCTGGG 421
QY 533 AGCAACAATGTTGTTTCCGGGAATGACAAACACGTCGTATCTGGGAATAACAACCAATGTG 592
DB 420 AGCACAATGTTGTTTCTGGGAACGACAACACTGTTCATATCCGGAACAACAACAATGTG 361
QY 593 TCTGGGAGCAACAACACTGTTGTTAACTGGAAGTGACAATATCTGTAGTGTGGTAGCAACAT 652
DB 360 GCTGGGAGCAACAACACTATCGTAACCGGGAACGACAATACCGTAACCTGGTAGCAACAT 301
QY 653 GTCGTATCAGGAGCAACAACATATCTGTATCTGGAGCAACAAGTCTGTATCCGGAACGAC 712
DB 300 GTCGTATCTGGGAGCAACAATATCTGTAACCAACAATGCGGTATCCGGGAATGAC 241
QY 713 AATAATGTCGTGGAAGTTCATATCTGATCAGGGAGCAACAATACCGTATCCGGGAGC 772
DB 240 AATAATGTCGTGGAAGTTCATATCTGGAAGCAACAATATCTGTATCTGGGAGC 181
QY 773 AACAACTGTATCCGGGAGCAACAATATCTGTATCTGGAGCAACAAGTCTGTATACAGAT 832
DB 180 AACAACTGTATCTGGGAACAACACTGTCGTATCTGGAGCAACAAGTCTGTAGAGAT 121
QY 833 GGTAAATAT-----TCTGTAGTGCAGGATGCTTCCATCTTCCCAAGTT 877
DB 120 GCATGATTTGTAAGTGGAGTGTCCATCTTCCGTGAGGAGCTCACCTTGTGTTCCGAGTT 61
QY 878 CAGTGTAGCTTCAATCAATAGATGAGACAAATCACTGTTATGTAACCTCA 927
DB 60 CGGTGTAGCTCAATCACTTGGTGGGCAATCGTGTATGTAACCTCA 11

RESULT 3

BJ461731/c

LOCUS

BJ461731

DEFINITION

vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone

baak46120 3', mRNA sequence.

ACCESSION

BJ461731

VERSION

BJ461731.1

KEYWORDS

EST.

BJ461731 686 bp mRNA linear EST 23-MAY-2002

BJ461731 K. Sato unpublished cDNA library, cv. Akashinriki

vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone

baak46120 3', mRNA sequence.

Accession

BJ461731

Version

BJ461731.1

Keywords

EST.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2005, 13:12:20 ; Search time 3171 Seconds
(without alignments)
11763.792 Million cell updates/sec

Title: US-10-657-852B-3
Perfect score: 980
Sequence: 1 gcttcattccaatcaaggt.....cccttacataaaaaaaaaa 980

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues 68479088

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
- 1: gb_est1:*
 - 2: gb_est2:*
 - 3: gb_hic:*
 - 4: gb_est3:*
 - 5: gb_est4:*
 - 6: gb_est5:*
 - 7: gb_est6:*
 - 8: gb_gss1:*
 - 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	372.8	38.0	767	4	BJ451048
C 2	372.4	38.0	746	4	BJ458554
C 3	370.2	37.8	686	4	BJ461731
C 4	370.2	37.8	699	4	BJ461803
C 5	366.6	37.4	687	4	BJ459099
C 6	365.6	37.3	693	4	BJ457564
C 7	365.6	37.3	696	4	BJ461908
C 8	362.4	37.0	588	2	BE490074
9	362.2	37.0	632	4	BJ453251
C 10	359.4	36.7	671	4	BJ454271
C 11	357.6	36.5	684	4	BJ462238
C 12	357.2	36.4	609	4	BJ450137
C 13	357.2	36.4	689	4	BJ458121
C 14	352	35.9	692	2	BF474043
C 15	348.2	35.5	703	2	BE705098
C 16	347	35.4	625	4	BJ448772
C 17	347	35.4	726	4	BJ451602
C 18	347	35.4	830	2	BE705403
C 19	346.4	35.3	663	4	BJ461352
C 20	344.4	35.1	830	2	BE705439
C 21	340.4	34.7	830	2	BE705439
C 22	335.6	34.2	1115	7	CK214468
C 23	332.6	33.9	841	4	BJ224369
C 24	331.6	33.8	851	4	BJ448689

C 25	328.8	33.6	675	4	BJ460799
C 26	325.4	33.2	724	4	BJ456413
C 27	323	33.0	620	4	BJ447068
C 28	322.2	32.9	589	1	AV909087
C 29	318.6	32.5	862	4	BJ454200
C 30	316.2	32.3	818	7	CK197682
C 31	310.8	31.7	775	2	BE705684
C 32	301.6	30.8	709	4	BJ453816
C 33	296.8	30.3	648	4	BJ300903
C 34	296	30.2	574	1	AV910970
C 35	294.6	30.1	914	7	CK156167
C 36	294	30.0	612	1	AV911379
C 37	293.6	30.0	581	4	BM376553
C 38	292.8	29.9	588	4	BJ453528
C 39	285	29.1	480	1	AJ460325
C 40	277.8	28.3	622	1	AU251218
C 41	275.8	28.1	585	4	BI479842
C 42	275	28.1	841	7	CK196896
C 43	263.2	26.9	532	2	BF200590
C 44	255.6	26.1	420	1	AJ460320
C 45	255.6	26.1	420	1	AJ460322

ALIGNMENTS

RESULT 1
BJ451048
LOCUS
DEFINITION
Bj451048 K. Sato unpublished cDNA library, cv. Akashinriki
vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone
baak32h16 5', mRNA sequence.
ACCESSION
BJ451048
VERSION
BJ451048.1 GI:21129647
KEYWORDS
EST.
SOURCE
Hordeum vulgare subsp. vulgare
ORGANISM
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE
1 (bases 1 to 767)
Sato, K., Saisho, D. and Takeda, K.
AUTHORS
Barley EST sequencing project in NIG and Okayama Univ
TITLE
Unpublished (2002)
JOURNAL
Contact: Tadasu Shin-i
COMMENT
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES

source
1..767
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Akashinriki"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="baak32h16"
/tissue_type="leaves"
/dev_stage="vegetative stage"
/clone_lib="K. Sato unpublished cDNA library, cv.
Akashinriki vegetative stage leaves"

ORIGIN

Query Match 38.0%; Score 372.8; DB 4; Length 767;
Best Local Similarity 73.5%; Pred. No. 4.2e-100;
Matches 524; Conservative 0; Mismatches 168; Indels 21; Gaps 3;
QY 233 GTGGATGCGAAACGACGACGCGCGTCTGGCGGTTTCGGCTCCCGAAGCGCGCTT 292
DB 27 GNAGCATCTTGGAGGCTTGCATGTTGGAGGAGCTCAACCTTGCACACACACTG 86

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CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
CC have a high nutritional value with reduced apical dominance or dwarfism,
CC early flowering or altered metabolic pathways. This sequence represents a
CC plant nucleic acid of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification but was obtained in
CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX

SQ Sequence 4536 BP; 1102 A; 1247 C; 1221 G; 965 T; 0 U; 1 Other;

Query Match	8.1%	Score 79.4;	DB 12;	Length 4536;
Best Local Similarity	63.1%	Pred. No. 2.2e-13;		
Matches 157;	Conservative 0;	Mismatches 86;	Indels 6;	Gaps 2;

QY	104	GCAACGTGCTGTCGTCCACACGACCTCCACGCGTTGAGGGCGCTCGCTGAGAAC	163
Db	76	GCTGCGGGCGGCATGCCACCCGGAGACCTCTCGCGCTGCGGGCATTTGCGGGGAAAT	135
QY	164	CT---AAGCGGCAAGAGCGCTCCGCTCCGCGCCGCGCATGTTCGCGCGCTCATGCTGC	220
Db	136	CTCTCTGCGGGTGGGGCGGCGCGGACTCCGCGCGCGTGTGCGGTGACGCCCTGCTGC	195
QY	221	AGCTGGGAAGGTGTGGATCGGAACAGCAAGCGGCGCGCTCGTGGCGTTGCGGCTCCCC	280
Db	196	GCCTGGGACGGCTCGCTCGGACGCGCGC---CGCCCGAGTCACGGCGCTGCGCCTCCCC	252
QY	281	AAGCGGCGCTTGGAGGATCATCCCATCGTCGATTGCTGAGCTTGATCACCTTCGCTAT	340
Db	253	GGGCGAGGTTCTGAGGGGGCCATCCCGCCCTCCTCGCGCCCTCGCGGCTCCAGGAC	312
QY	341	TTGGATCTC	349
Db	313	CTGACCTC	321

Search completed: October 8, 2005, 17:53:50
Job time : 580 secs

PD 18-MAR-2004.
 XX 09-SEP-2003; 2003WO-NZ000199.
 XX 09-SEP-2002; 2002US-0409557P.
 PR (GENE-) GENESIS RES & DEV CORP LTD.
 PA (WRIGHT-) WRIGHTSON SEEDS LTD.
 XX Demmer J, Shenk MA, Hall C, Fish SA;
 XX WPI; 2004-248453/23.
 DR P-PSDB; ADM41471.
 XX New antifreeze proteins and encoding polynucleotides, useful for
 PT modulating cold tolerance in organisms, as food additives, or for
 PT treating tumors or disorders associated with the presence of unwanted
 PT biocrystals (e.g. gout).
 XX Claim 1; SEQ ID NO 1; 71pp; English.
 XX The present sequence is that of cDNA encoding APPI, an antifreeze protein
 CC of perennial ryegrass. The cDNA was isolated from a pseudostem cDNA
 CC expression library. The invention provides forage grass (perennial
 CC ryegrass and tall fescue) antifreeze proteins and the polynucleotides
 CC encoding them ADM41458-ADM41483. The polynucleotides were isolated from
 CC tissues taken at different times of year (winter and spring) and from
 CC different parts of the plants. The polynucleotides can be used to
 CC modulate the cold tolerance of an organism, especially plants, mammals,
 CC insects, fungi, archaea and bacteria. The method involves incorporating
 CC an antifreeze polynucleotide, under the control of a gene promoter
 CC sequence, into the genome of the organism, or introducing double-stranded
 CC RNA corresponding to the polynucleotide into the cells of the organism,
 CC thereby inhibiting expression of an antifreeze polypeptide. The
 CC antifreeze protein can be used for the cryopreservation of a cell or
 CC tissue, as a food additive of a frozen food product, in a method for
 CC decreasing the time required to dehydrate a composition, to treat a
 CC disorder characterised by biocrystals associated with disorders such as
 CC gout and kidney stones, to preserve the viability of a molecular biology
 CC reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and
 CC to protect a plant from damage due to frost or freezing.
 XX Sequence 841 BP; 216 A; 217 C; 222 G; 186 T; 0 U; 0 Other;
 SQ
 Query Match 26.8%; Score 262.2; DB 12; Length 841;
 Best Local Similarity 73.5%; Pred. No. 3.1e-71;
 Matches 349; Conservative 0; Mismatches 123; Indels 3; Gaps 1;
 QY 380 AAAAGTTTCAGATACGGCTCAAGAGCCTCACCACTGACAGCCAGTCACTCGGTATGGT 439
 DB 262 AAGAGCTTCCAGATATGCTCAAGAGGCTCACCGCGCTGCGGTCTGCTGGTAAGCG 321
 QY 440 TCATTAAACATGCTATGTCATGTGAGCAGTAG---AAGAACGCTCGATGAAGAACCAAT 496
 DB 322 TTCACTACATGCCATTATCATGTGAAGCCTAGCAGGAACACTCGACGAGACCAAT 381
 QY 497 ACAATATCAGGACCAACAATAGTGTGATCAGGAGCAACAATGTTTTCGGGAT 556
 DB 382 ACAATAACTGGGATCAACAATATCTGTGATCGGAGCAACAATGTTTTCGGGAT 441
 QY 557 GACACACGGTCTGTCTCGGATACCAACCACTGTCTGGAGCAACAACACTGTGTA 616
 DB 442 GATACACTGTATATCCGGGACCAACAACGTCGTGTCGGGAGCCACAACCGTGTGA 501
 QY 617 ACTGGAAGTGACAATCTAGTGTGATGAGCAACCACTGCTATCAGGAGCAACAAGCATAT 676
 DB 502 TTTGGGGTGACAACATTCATAGTGAAGTACCATGTCGTATCTGGAACCAACCATGTT 561
 QY 677 GTTACTGATACAAATATGTTGATCCGGGAGCAACAATATGTTGTCGGAAGCTTCCAT 736
 DB 562 GTGACTGACAACAAGAAATCCGTTATCCGGGGAGCCACAATCTGTATCTGGAAGCAAAAT 621
 QY 737 ACTGTATCAGGAGGAGCACAATACCGTATCCGGGAGCAACAATCTGTATCTCGGGAGCAAC 796

DB 622 ACCGTATCCGGAGACCAACAGATCGTATCTGGAGCCACAGTACGTATCCGGAGCAAC 681
 QY 797 CATATCGGTATCTGGAGCAACAAGAGTCTGAACAGATGTTTAAATATCTTCTAGGTG 851
 DB 682 AATACGGTATCTGGAGAAACAATTCCTGATATATGGGAACAACAATATTTGTATCTG 736
 RESULT 15
 ADJ40496
 ID ADJ40496 standard; cDNA; 4536 BP.
 XX AC
 XX ADJ40496;
 XX DT 06-MAY-2004 (first entry)
 XX DE Plant cDNA #1496.
 XX KW Plant; gene; ss; transcription; plant genome augmentation; cereal;
 KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
 KW maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
 KW stress tolerance; salt tolerance; cold tolerance; drought tolerance;
 KW plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
 KW antifungal.
 XX OS Eukaryota.
 XX PN US2004016025-A1.
 XX PD 22-JAN-2004.
 XX PF 26-SEP-2002; 2002US-00260238.
 XX PR 26-SEP-2001; 2001US-0325277P.
 PR 26-SEP-2001; 2001US-0325448P.
 PR 04-APR-2002; 2002US-0370620P.
 XX (BUDW//) BUDWORTH P.
 PA (MOUG//) MOUGHAMER T.
 PA (BRIG//) BRIGGS S P.
 PA (COOP//) COOPER B.
 PA (GLAZ//) GLAZEBROOK J.
 PA (GOFF//) GOFF S A.
 PA (KATA//) KATAGIRI F.
 PA (KREP//) KREPS J.
 PA (PROV//) PROVART N.
 PA (RICK//) RICKE D.
 PA (ZHUT//) ZHU T.
 XX Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;
 PI Goff SA, Katagiri F, Kreps J, Provart N, Ricke D, Zhu T;
 XX WPI; 2004-190374/18.
 DR New rice promoter, useful for manipulating crop plants to alter or
 XX improve phenotypic characteristics, e.g. produce large quantities of oil
 PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
 PT or high nutritional value.
 XX Claim 25; SEQ ID NO 1496; 230pp; English.
 XX The invention relates to plant nucleotide sequences that direct seed-,
 CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
 CC or constitutive transcription of an operatively linked nucleic acid
 CC segment. The invention also relates to a method for augmenting a plant
 CC genome and a method of identifying a gene, where its expression is
 CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
 CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
 CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
 CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
 CC encode are useful for manipulating crop plants to alter or improve
 CC phenotypic characteristics, to produce large quantities of oil or
 CC proteins, to incur resistance to insecticides, viruses or fungi, and to

Qy	383	AGTTTGCAGATACGGCTCAAGAGCCTCACCACTGACAGCCAGTCTACTCGGTATGGGTCC	442
Db	292	AGTTTCCAGATATTCTCAAAAGGGCTCACACCGCTGCGCGTCTCACTGGGTAAAGCGCTTC	351
Qy	443	ATTAAACATGCTATTGCATGTGACAGTAG--AAGAACGCTCGATGAGAACCAAAATACA	499
Db	352	ACTAACATGCCATTACATGTGAAGTCTTAGCCAAAGAACACTCGACGAAGAACACAAATACA	411
Qy	500	ATATCAGGGACCAACAATAGTGTTCGATCAGGGAGCAACAATGTGTTCCTCCGGGAATGAC	559
Db	412	ATACTGGGATCAACAATACTGTCAAATCCGGGAGCAACAATGTGTTCCTGGGAACGAT	471
Qy	560	AACACGGTCTGATCTGGGAATAACAACCATGTGTCTGGGAGCAACAACACTGTTGTAATC	619
Db	472	AACACTGTCTATCCGGGAACAACAACGTCGTGTCCGGGAGCCACAACAACCGTCGTATTT	531
Qy	620	GGAAGTGACAATACTGTGTAGTTGGTAGCAACCATGTGTCATCAGGGAGCAAGACATATTGTT	679
Db	532	GGGGGTGACAAATTTCTAAGCGGTAGCAACCATGTGTCATCTCTGGGAACCAACCATGTCGTG	591
Qy	680	ACTGATAACAATAATGTTGTATCCGGGAACGACAATAATGTCTCTGGAAGCTTCACATCT	739
Db	592	ACTGACAAACAAGATGCCGTATCCGGGAGCCACAATACTGTATCTGGAAAGCCAAATATCC	651
Qy	740	GTATCAGGGGAGCACAATACCGTATCCGGGAGCAACAATACTGTATCCGGGAGCAACCAT	799
Db	652	GTATCCGGGAACCAATATCATATCTCGAGCCACAGTACCATATCCGGGAACCAACAT	711
Qy	800	ATCGTATCTGGGAGCAACAAGTCGTAAACAGATGTTTAATATTCTGTAGGTG	851
Db	712	ACCGTATCTGGGAGCAACAATTTCTGTATCTGGGAACAACAATATTGTGATCTG	763

RESULT 13	
AAAX99717	
ID	AAAX99717 standard; DNA; 357 BP.
XX	
XX	AAAX99717;
XX	
XX	29-SEP-1999 (first entry)
DT	
XX	
XX	Grass anti-freeze protein coding sequence.
XX	
XX	Anti-freeze protein; grass; plant; frozen food product; frost tolerance;
KW	frozen confectionery; ss.
KW	
XX	
XX	Lolium perenne.
OS	
XX	
XX	WO9937782-A2.
PN	
XX	
XX	29-JUL-1999.
PD	
XX	
XX	23-DEC-1998; 98WO-EP008553.
PF	
XX	
XX	22-JAN-1998; 98GB-00001408.
PR	
XX	
XX	(UNIL) UNILEVER NV.
PA	
PA	(UNIL) UNILEVER PLC.
XX	
XX	Jarman CD, Sidebottom CM, Twigg S, Worrall D;
PI	
XX	
XX	WPI: 1999-458697/38.
DR	
DR	P-PSDB; AAY22472.
DR	
XX	
XX	New plant anti-freeze protein useful in frozen food products.
PT	
XX	
XX	Claim 8; Page 37; 39pp; English.
PS	
XX	
XX	This sequence encodes the plant anti-freeze protein of the invention. The
CC	anti-freeze protein is characterised in that at least 40% of its amino
CC	acids are from the group of serine, threonine and asparagine. The anti-
CC	freeze protein can be used in frozen food products, especially frozen
CC	

CC	confectionery. Anti-freeze proteins are especially used in food products,
CC	which are heated, e.g. by pasteurisation, blanching or sterilisation
CC	prior to freezing. Plants transformed with a nucleic acid sequence
CC	encoding the anti-freeze protein have an increased frost tolerance. Prior
CC	art anti-freeze proteins have not been applied to commercially available
CC	food products, due to high costs and complicated processes for obtaining
CC	the protein. Also prior art anti-freeze proteins have tended to
CC	destabilise during processing especially during the pasteurisation step.
CC	This is overcome by the present anti-freeze protein. The anti-freeze
CC	proteins provide an ice particle size following an ice recrystallisation
CC	inhibition assay of 15 µm M or less. The anti-freeze protein ingredient
CC	means that mixes can be frozen under quiescent conditions, e.g. in a shop
CC	or home freezer without the formation of unacceptable ice crystal shapes
CC	and hence with a texture different to products normally obtained via
CC	quiescent freezing
XX	
SQ	Sequence 357 BP; 116 A; 80 C; 89 G; 72 T; 0 U; 0 Other;
Query Match 27.0%; Score 264.2; DB 2; Length 357;	
Best Local Similarity 83.8%; Pred. No. 4.4e-72;	
Matches 299; Conservative 0; Mismatches 58; Indels 0; Gaps 0;	
QY	482 GATGAAGACCAATACATATCAGGACCCCAACAATAGTGTGGATCAGGAGCAACAAT 541
DB	1 GATGAACAGCCGAATACGATTTCTGGAGGCAACAATCTGTTCAGATCCGGAGCAAAAAT 60
QY	542 GTTGTGTTCCGGGAATGACAAACCGTTCGTATCTGCGGAATAACAACCATGTGTCGGGAGC 601
DB	61 GTTCTGCTGGGAATGACAAACCGTCATATCTGGGGACACAATAGTGTGTCGGGAGC 120
QY	602 AACAACTGTTGTAACCTGAAGTGACAAATCTGTGTAGTTGGTAGCAACCAATGTCGTATCA 661
DB	121 AACAACTGTCGTAAGTGGGAATGACAAATCCGTAAACCGGACCAACCATGTGTCGTATCA 180
QY	662 GGCACAAAGCATATTGTTACTGTATACAAATAATGTTGTATCCGGGAACGACAAATATGTCG 721
DB	181 GGCACAAACCATATCGTTTACAGACAAACAATAACGTATCCGGGAACGATAATAATGTA 240
QY	722 TCTGGAAGCTTCCATCTACTGTATCAGGGGAGCAACAATACCGTATCCGGGAGCAACAATCT 781
DB	241 TCCGGGAGCTTTCATACCGTATCCGGGGGACAAATCTGTGTCCGGGAGCAACAATACC 300
QY	782 GTATCCGGGAGCAACCATATCGTATCTGGGAGCAACAAAGTCGTAAACAGATGTTAA 838
DB	301 GTATCTGGGAGCAACCAACCGTTGTATCTGGAAGCAACAAAGTCGTGACAGACGCTTAA 357
RESULT 14	
ADM41458	
ID ADM41458 standard; cDNA; 841 BP.	
XX	AC ADM41458;
XX	XX
DT	03-JUN-2004 (first entry)
DE	Perennial ryegrass antifreeze protein AFPI cDNA.
XX	XX
KW	Antifreeze; perennial ryegrass; cold tolerance; transgenic; plant;
KW	antigout; litholytic; nephrotropic; cytostatic; gene; ss.
XX	XX
OS	Lolium perenne.
XX	XX
PH	Key Location/Qualifiers
FT	CDS 55..786
FT	/*tag= b
FT	/product= "Antifreeze protein AFPI"
FT	55..114
FT	/*tag= a
FT	mat_peptide 115..783
FT	/*tag= c
XX	XX
XX	WO2004022700-A2.
PN	XX

Best Local Similarity 70.3%; Pred. No. 6e-120;		Matches 701; Conservative 0; Mismatches 206; Indels 90; Gaps 7;	
Qy	33	CCATGCTGAATACATGGCAAGTGTTCATGCTGCTCTTCTTGGGGTTCACTTGC	92
Db	46	CCAGAACTTAATCCATGGCGAAATGTTGGCTGCTCTTCTTGGTGTCTCTTGC	105
Qy	93	AGTGTGCAGGAGCAACGTGCTGCTGTGCACCAACGACGACCTCCACGCGTTGAGGGGC	152
Db	106	TGGCCATGAGCGGAC-----GTGCTGCACCTGGATGACCTCCGCGGCTGCGGGGT	159
Qy	153	TCGCTGAGAACCTTAACGCGCAAGAGCCGTCCGCTCCGCGCGCATGGTCCGCGCT	212
Db	160	TTGTGCGGAACCTCAATGCG---GGGGTGCCCTTCTCGGTGGAACATGCTCTGGCTCT	216
Qy	213	CATGCTGACGCTGGGAGGTGTGGATGCGAAACAGCAGCGCGCGCTGTTGGCGTTGC	272
Db	217	CATGCTGCGATTGGGAAAGTGTGGCTGCGATGGTACAAGCGCGCGCTCACGGCGTTGC	276
Qy	273	GGCTCC-----CCAGCGCG	287
Db	277	GGCTTCGGATTAGCTCGAGGACTGCGGTAAGCTCAAGTCGCTCAACCTTGCACGAAA	336
Qy	288	GGCTTGGAGGGATCATCCCATCGTCGATTGGTGAGCTTGGATCACCTTCGCTATTGGATC	347
Db	337	GATTGGTTGGCACCATCCCGTCGTGGATTGGTGAGCTTGACCACCATTCGTACTTGGTTC	396
Qy	348	TCTCGGGTAATTCATTGGTTGGGAGGTACC-----AAAAAGTTTCGAGATAC	395
Db	397	TCTCGGATAATTCATTGGTTGGTAAGCCACCAATAGTTTGACCAATAGTTTGCAGATAA	456
Qy	396	GGCTCAAGAGCTCACCACCTGACAGCAGTCACCTCGGTATGGTTCCATTACATGCTAT	455
Db	457	GACTCAAGGCGCTCGCCACCGCTGCTGTTCACTAGGTATGGCTTTCGCTAACATGCCAT	516
Qy	456	TGCATGTGA---GCAGTAGAAGACGCTCGATGGAAGAACCAATACAATATCAGGACCA	512
Db	517	TGCATGTGAAGGGACCGAAGACCCTCGACGAACAACAATAACATACATGGACCA	576
Qy	513	ACAATAGTTGGATCAGGAGCAACAATGTGTTTTCGGGAATGACAAACAGGTGATAT	572
Db	577	ACAACACTGTAGATCTGGGAACGACAATGCTGTTTCTGGGAACGACAACACTGTATAT	636
Qy	573	CTGGGAATACACCACTGTCTGGGAGCAACAACACTGTTGTAAGTGAAGTGAATA	632
Db	637	GTGGGAACAACAACACTGTGCTGGGAGCAACAACCAATTCATCTCGCAGTGACAATA	696
Qy	633	CTGTAGTTGGTAGCAACCATGCTATCAGGACAAAGCATATTGTTACTGATAACAATA	692
Db	697	TGCTAACTGGCAGCAACCATATTGATGTGGACCAACAACATATCATATGATACAA	756
Qy	693	ATGTTGTATCCGGGAACGACAATAATGTGTCTGGAAAGTTCCTACTGTATCAGGGAGC	752
Db	757	ATGACGTATCCGCAATGATAATAATGTATCTGGGAGCTTCCATCTACTGTATCCGGAGCC	816
Qy	753	ACAATACCTATCCGGAGCAACAATATCTATCCGGGAGCAACCATCTGATCTGGGA	812
Db	817	ACAATACTGTATCTGGAAGTACAACACTGTATCTGGAAGCAACCAATGCTGATCTGGAA	876
Qy	813	GCAACAAAGTCGTAACAGATGGTTAATATCTGTAGG-----TGC	852
Db	877	GCACAAACTGTGACAGAGATGAATGATTTGTACAGGGATGCTTCCATCTTCTTAA	936
Qy	853	AGGATTGCTTCCATCTTCCCAAGTTCAGTGTAGCTTTACAAATCAATAGATGGAGACAATCA	912
Db	937	AGGAGCTCTCACCTAGTCCAAAGTTCGGTGCAGCTCACAATCACTTGGTAGGACAATCG	996
Qy	913	CGTTATGTAACITCA--GGATATGGGATACTTTTCCTT	948
Db	997	AGTTATGTAACTTCATGGGATAGCATCATCTTCCTCCT	1033

ADM41465	ADM41465 standard; cDNA; 1064 BP.		
ID	ADM41465		
XX	AC	ADM41465;	
XX	DT	03-JUN-2004 (first entry)	
XX	DE	Perennial ryegrass antifreeze protein APP4 cDNA.	
XX	KW	Antifreeze; perennial ryegrass; cold tolerance; transgenic; plant;	
XX	KW	antigout; litholytic; nephrotropic; cytostatic; gene; ss.	
OS	Lolium perenne.		
XX	Key	Location/Qualifiers	
FH	CDS	55..897	
FT		/*tag= b	
FT		/product= "Antifreeze protein APP4"	
FT	sig_peptide	55..120	
FT		/*tag= a	
FT	mat_peptide	121..894	
FT		/*tag= c	
XX	WO2004022700-A2.		
XX	PN		
XX	PD	18-MAR-2004.	
XX	PP		
XX	PF	09-SEP-2003; 2003WO-NZ000199.	
XX	PR		
XX	PR	09-SEP-2002; 2002US-0409557P.	
XX	PA	(GENE-) GENESIS RES & DEV CORP LTD.	
XX	PA	(WRIG-) WRIGHTSON SEEDS LTD.	
XX	PI	Demmer J, Shenk MA, Hall C, Fish SA;	
XX	PI		
DR	WPI; 2004-248453/23.		
DR	P-PSDB; ADM41478.		
XX		New antifreeze proteins and encoding polynucleotides, useful for	
XX	PT	modulating cold tolerance in organisms, as food additives, or for	
XX	PT	treating tumors or disorders associated with the presence of unwanted	
XX	PT	biocrystals (e.g. gout).	
XX	PS	Claim 1; SEQ ID NO 8; 71pp; English.	
XX	PS		
CC	CC	The present sequence is that of cDNA encoding APP4, an antifreeze protein	
CC	CC	of perennial ryegrass. The cDNA was isolated from a leaf and pseudostem	
CC	CC	cDNA expression library. The invention provides forage grass (perennial	
CC	CC	ryegrass and tall fescue) antifreeze proteins and the polynucleotides	
CC	CC	encoding them ADM41458-ADM41483. The polynucleotides were isolated from	
CC	CC	tissues taken at different times of year (winter and spring) and from	
CC	CC	different parts of the plants. The polynucleotides can be used to	
CC	CC	modulate the cold tolerance of an organism, especially plants, mammals,	
CC	CC	insects, fungi, archaea and bacteria. The method involves incorporating	
CC	CC	an antifreeze polynucleotide, under the control of a gene promoter	
CC	CC	sequence, into the genome of the organism, or introducing double-stranded	
CC	CC	RNA corresponding to the polynucleotide into the cells of the organism,	
CC	CC	thereby inhibiting expression of an antifreeze polypeptide. The	
CC	CC	antifreeze protein can be used for the cryopreservation of a cell or	
CC	CC	tissue, as a food additive of a frozen food product, in a method for	
CC	CC	decreasing the time required to dehydrate a composition, to treat a	
CC	CC	disorder characterised by biocrystals associated with disorders such as	
CC	CC	gout and kidney stones, to preserve the viability of a molecular biology	
CC	CC	reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and	
CC	CC	to protect a plant from damage due to frost or freezing.	
XX			
SQ	Sequence 1064 BP; 263 A; 274 C; 267 G; 260 T; 0 U; 0 Other;		

Query Match

Best Local Similarity

Matches

711: Conservative

40.2%; Score 394.4; DB 12; Length 1064;

67.2%; Pred. No. 1e-112;

0; Mismatches 226; Indels 121; Gaps 6

Query Match 40.2%; Score 394.4; DB 12; Length 1064;
Best Local Similarity 67.2%; Pred. No. 1e-112;
Matches 711; Conservative 0; Mismatches 226; Indels 121; Gaps 6;

CC different parts of the plants. The polynucleotides can be used to
CC modulate the cold tolerance of an organism, especially plants, mammals,
CC insects, fungi, archaea and bacteria. The method involves incorporating
CC an antifreeze polynucleotide, under the control of a gene promoter
CC sequence, into the genome of the organism, or introducing double-stranded
CC RNA corresponding to the polynucleotide into the cells of the organism,
CC thereby inhibiting expression of an antifreeze polypeptide. The
CC antifreeze protein can be used for the cryopreservation of a cell or
CC tissue, as a food additive of a frozen food product, in a method for
CC decreasing the time required to dehydrate a composition, to treat a
CC disorder characterised by biocrystals associated with disorders such as
CC gout and kidney stones, to preserve the viability of a molecular biology
CC reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and
CC to protect a plant from damage due to frost or freezing.

XX SQ Sequence 1007 BP; 252 A; 265 C; 253 G; 237 T; 0 U; 0 Other;

Query Match 50.3%; Score 492.8; DB 12; Length 1007;
Best Local Similarity 73.6%; Pred. No. 1.2e-143;
Matches 739; Conservative 0; Mismatches 197; Indels 68; Gaps 6;

QY 12 AATCAAGGTTTCTTGTCAATCCATGCTGTAATACATGCAAAAGTGTTCATGCTGCTGG 71
DB 37 ATTGAATCCATCTATAGCATAGCACTGCTGTAATCCATGGCGAAATGCTTGATGCTGCTTC 96
QY 72 TCTTCTGGGGTTCATCTTGGAGTGGCAGGA-----GCAAGTGTGCTGCTGCC 122
DB 97 TCTCCTTCGCTTCTTGTTCGGGGCCGCGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 156
QY 123 ACCAGACGACCTCCACGCGGTTGAGGGGCTCGCTGAGAACCTAAGCGGCAAGAGGCGG 182
DB 157 ACGCGATGACCTTCGCGGCTGCGGGGCTTCTGTGAGAACCTGGCGGCGGCGGCGGCGGCGG 216
QY 183 TCGCCTCCGCGCGCATGCTCGGCGCTCATGCTGACGCTGGGAGGTGTGGAGTGG 242
DB 217 TCAGCCTCCGCGCGGCTGCTCAGGCGCTCATGCTGCGATTGGGAAGGCGTTGGCTGG 276
QY 243 AAACAGCAAGCGCGCGCTGCTGGGCTCCGAGCGCGGCTCCGAGCGCGGCTTGGAGGATCA 302
DB 277 ACGGTGCCAGCGCGCGCTGTCAGGGCTTGTGGCTCCCGAGGAGCGCGGCTTCCAGCGGCGCAA 336
QY 303 TCCCATCGTGTGCTGAGCTGATCACCTTCGCTATTGATCTCTCGGGTAATTCAT 362
DB 337 TCCGTCATGATTTTTCAGCTTCCACCTACCTAGCTACTTGATCTTTTCAGTATGCTAT 396
QY 363 TGGTTGGGAGGTACCAAAAGTTTGCAGATAGGCTCAAGAGCCTCACCACTGCAGCGC 422
DB 397 TGGTTGGGAGGTACCAAGATCTCAGGTACAGCTCAAAGGCATCAC-----446
QY 423 AGTCACTCGGTATGGGTTCCATTAACATGCTATTGATGTGA---GCAGTAGAGAACGC 479
DB 447 -----AACATGCCATTGCTATGCTGATGCGGTAACAGAGATCAC 483
QY 480 TCGATCAAGAACCAATAACAATACAGGACCAACAATAGTTGATCAGGAGGAGCAACA 539
DB 484 TCGACGAGCGCCCAATACATTTCTGGGAGCAACAATACTGTCAATCGGAGGAGCAAAA 543
QY 540 ATGTTGTTTTCGGGAATGACCAACACGCTGTGATCTCGGGAATAACAACCATGTGTGGGA 599
DB 544 ATGTTCTTGTGGGAATGACCAACACGCTGTGATCTCGGGAACAATAAGTGTGTCTGGGA 603
QY 600 GCAACAACACTGTTGTAACCTGGAAGTGACAACTACTGTAGTTGGTACCAACCATGTGTTAT 659
DB 604 GCAACAACACTGTCGTAAGTGGGAATGACAATAACCGTAAACCGGACGACCAATGTGTTAT 663
QY 660 CAGGGAACAAGCATATTGTTACTGATAACAATAATGTTGATCCGGGAACGACAAATAATG 719
DB 664 CAGGGAACAACCATATCTGTTTACAGCAACAACAATACGTTATCCGGGAACGATATATG 723
QY 720 TGTCTGGAAGCTTCCATCTACTGTATCAGGGGAGCACAATACCGTATCCGGGAGCAACAATA 779
DB 724 TATCCGGGAGCTTTCATACCGTATCCGGGGGCGACAACTACTGTCTCCGGGAGCAACAATA 783

QY 780 CTGTATCGGAGCAACCATATCGTATCTGGAGCAACAAAGTCGTAAACAGATGTTTAA 839
DB 784 CCGTATCTGGAGCAACACCGTTGTAICTGGAAGCAACAAAGTCGTGACAGCGCTTAA 843
QY 840 ATTCTGTAGGTGCGAGGATGTTCCATTT-----CCCAAGTTCAG 880
DB 844 GATCTGTGAGCGCATGATTGTTTCCACCTTAACTGAGCTCAGGTTCTTTGTCCCAAGTTCAC 903
QY 881 TGTAGCTTACATCAATAGATGGAGACATCAGGTTATGTAACCTTCA--GGATATGGCATA 939
DB 904 TGTACCTCACAGTCAGTTGGTGGCTTCAATCGCGTTAIGTAACTTCATGATATACCATA 963
QY 940 CTTTTC-----CTTTAAATAAAGCTTCCCTTTTACATAAAAAAAA 980
DB 964 CTTTTCCTACTATATATAAATTTCCCTTTTACATAAAAAAAA 1007

RESULT 6

ADM41463

ID ADM41463 standard; cDNA; 1230 BP.

XX AC ADM41463;

XX DT 03-JUN-2004 (first entry)

XX Tall fescue antifreeze protein cDNA.

XX Antifreeze; fescue; cold tolerance; transgenic; plant; antigout;

XX litholytic; nephrotropic; cytotstatic; gene; ss.

XX Schedonorus arundinaceus.

XX Key Location/Qualifiers

XX CDS 76..909

XX /*tag= b

XX /product= "Antifreeze protein"

XX sig_peptide 76..141

XX /*tag= a

XX mat_peptide 142..906

XX /*tag= c

XX WO2004022700-A2.

XX 18-MAR-2004.

XX 09-SEP-2003; 2003WO-NZ0000199.

XX 09-SEP-2002; 2002US-0409557P.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX (WRIG-) WRIGHTSON SEEDS LTD.

XX Demmer J, Sherk MA, Hall C, Fish SA;

XX WPI: 2004-248453/23.

XX P-PSDB; ADM41476.

XX New antifreeze proteins and encoding polynucleotides, useful for
PT modulating cold tolerance in organisms, as food additives, or for
PT treating tumors or disorders associated with the presence of unwanted
PT biocrystals (e.g. gout).

XX Claim 1; SEQ ID NO 6; 71pp; English.

CC The present sequence is that of cDNA encoding an antifreeze protein of
CC tall fescue. The invention provides forage grass (perennial ryegrass and
CC tall fescue) antifreeze proteins and the polynucleotides encoding them
CC ADM41458-ADM41483. The polynucleotides were isolated from tissues taken
CC at different times of year (winter and spring) and from different parts
CC of the plants. The polynucleotides can be used to modulate the cold
CC tolerance of an organism, especially plants, mammals, insects, fungi,
CC archaea and bacteria. The method involves incorporating an antifreeze
CC polynucleotide, under the control of a gene promoter sequence, into the

ryegrass and tall fescue) antifreeze proteins and the polynucleotides encoding them ADM4158-ADMA41483. The polynucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polynucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze polypeptide. The antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by bicrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to frost or freezing.

Sequence 1008 BP; 256 A; 265 C; 251 G; 236 T; 0 U; 0 Other;

SQ Sequence 1008 BP; 256 A; 265 C; 251 G; 236 T; 0 U; 0 Other;

Query Match 51.4%; Score 503.6; DB 12; Length 1008;
Best Local Similarity 74.3%; Pred. No. 4.7e-147;

Qy	12	AATCAAGGTTTCTTGTTCATATCCATGCTCGATGATCATGGCAAAAGTGTGGATGCTGCTGG	71
Db	44	ATTGAATCCATCTTATAGCATAGCACTGTGTAATCCATGGCGAAATGCTTGTATGCTGCTGC	103
Qy	72	TCTTCTTTGGGTTTCATCTTGCAGTGGCAGGA--GCAACGTGCTGGTCTGTCGCCACACG	128
Db	104	TCTCTTTCGCGTTCTCTTTGCTGGTGGCGACGGCGACGGCGACCATGCCACCGCG	163
Qy	129	ACGACCTCCACGCTTGAGGGGCTTCGTGAGAACCTAAGCGGAAAGAGCGCTCCGCC	188
Db	164	ATGACCTTCGCGCGCTTCGGGGCTTCGTGAGAACCTGGGCGGGCGCGCAATCAGCC	223
Qy	189	TCCGCGCGCATGTTCCGGCGCCTCATGCTCGAGCTGGGAAGGTGTGGGATGCGGAAACAG	248
Db	224	TCCGCGCGCGTGTTCAGGCGCCTCATGCTCGATTGGGAAGGCGTTGGCTCGCAGCGTG	283
Qy	249	CAAGCGGCGCGTTCGTGGCGTTGGGCTCCCAAGCGGGGCTTTGGAGGGATCATCCCAT	308
Db	284	CCAGCGCGCGTGTCAAGGCTTTGTGGCTCCCGAGGAGCGGCTCACGGGGCGCAATCCCGT	343
Qy	309	CGTCGATTGGTGAGCTTGATCACCTTCGCTATTTTGGATCTCTCGGTAATTCATTGGTTG	368
Db	344	CATGATTTGTACGTTTCACACCTACGCTACTTTGGATCTTTTCAAGTAATGATTTGGTTG	403
Qy	369	GGGAGGTACCAAAAAGTTTGAGATACGGCTCAAGAGCCTCACCACTGACAGCCAGTCAC	428
Db	404	GCAGGTTACCCAAGAACTGCGAGTACAGCTCAAAGGCATCACC-----	447
Qy	429	TCGGTATGGGTTTCATTAAATGCTATTGGATGTGA---GCAGTAGAAGAACGCTCGATG	485
Db	448	-----AACATGCCATTGCAATGTGATGCGTTAACAGAAAGATCACTTCGACG	490
Qy	486	AAGAACCAATACAAATACAGGACCAACAATAGTGTGGATCAGGGAGCAACAATGTTG	545
Db	491	AGACGCCAATACAAATTTCTGGGAGCAACAATCTGTCAAGTCCGGGAGCAAAAATGTT	550
Qy	546	TTTTCCGGGAATGACAAACACGGTCTGTATCTGGGAATAACAAACATGTGTCTGGGAGCA	605
Db	551	TTGCTGGGAATGACAAACACCGTCATATCTGGGGACAACAATAGTGTGTCTGGGAGCA	610
Qy	606	ACATGTTGTAACTGGGAAGTGACAATACTGTAGTTGGTAGCAACAATGTCGTATCAGGGA	665
Db	611	ACATGTCGTAAGTGGGAAATACAAATACCGTTAACCGGCAGCAACCATGTCTGTATCAGG	670
Qy	666	CAAGCATATTGTTACTGATAACAATAATGTTGTATCCGGGAAACGACAAATATGTGCTG	725
Db	671	CAAAACCATATCGTTACAGACAAACAATAACGTTATCCGGGAAACGATAATATGTATCCG	730
Qy	726	GAAGCTTCCATCTGTATTCAGGGGAGCAACAATACCGTATCCGGGAGCAACAATACTGTAT	785

CC The present sequence is that of cDNA encoding an antifreeze protein of
 CC tall fescue. The cDNA was isolated from a leaf blade cDNA expression
 CC library. The invention provides forage grass (perennial ryegrass and tall
 CC fescue) antifreeze proteins and the polynucleotides encoding them
 CC ADMA1458-ADMA1483. The polynucleotides were isolated from tissues taken
 CC at different times of year (winter and spring) and from different parts
 CC of the plants. The polynucleotides can be used to modulate the cold
 CC tolerance of an organism, especially plants, mammals, insects, fungi,
 CC archaea and bacteria. The method involves incorporating an antifreeze
 CC polynucleotide, under the control of a gene promoter sequence, into the
 CC genome of the organism, or introducing double-stranded RNA corresponding
 CC to the polynucleotide into the cells of the organism, thereby inhibiting
 CC expression of an antifreeze polypeptide. The antifreeze protein can be
 CC used for the cryopreservation of a cell or tissue, as a food additive of
 CC a frozen food product, in a method for decreasing the time required to
 CC dehydrate a composition, to treat a disorder characterised by biocrystals
 CC associated with disorders such as gout and kidney stones, to preserve the
 CC viability of a molecular biology reagent, to destroy unwanted tissue in a
 CC patient e.g. tumour tissue, and to protect a plant from damage due to
 CC frost or freezing.

XX SQ Sequence 1006 BP; 248 A; 261 C; 260 G; 237 T; 0 U; 0 Other;

Query Match 55.3%; Score 541.6; DB 12; Length 1006;
 Best Local Similarity 76.5%; Pred. No. 5.3e-159;
 Matches 756; Conservative 0; Mismatches 194; Indels 38; Gaps 6;

QY 22 TCTGTTCATCATCGCTGGAATACATGCGCAAGTGTTCATGCTGCTGCTTCTTGGG 81
 DB 28 TCTATAGCATAGCACTGCTGTAATCCATGCGCAATGCTGTGCTGCTCTCTCGC 87
 QY 82 GTTCATCTGAGGTGGCAGGA---GCAACGTGCTGCTGCTGCCACCGACACTCCA 138
 DB 88 GTTCTCTTGTGCGCGCTGGCAGCGCGACCGCATCCACCGGATGACTCG 147
 QY 139 CGCTGTGAGGGCTCGCTGAGAACCTTAAGCGCAAGAGCGCTCCGCTCCGCGCGC 198
 DB 148 TCGCTGCGGGGTTCCGTGAGAACCTGGCGCGCGCGCACTCAGCTTCGCGCGC 207
 QY 199 ATGTCGCGCGCTCATGCTGAGCTGGGAAGTGTGGATGCGAAACGAAGCGCG 258
 DB 208 GTGGTCAGCGCTCATGCTGCGATTGGGAAGCGTGTGCTGCGAGGTGCCAGCGCG 267
 QY 259 CGTGTGCGGTTGCGGCTCCCAAGCGGCTTGGAGGATCATCCATCTCGATTGG 318
 DB 268 TGTCAAGGCTTTGTGCTCCCGAGGAGCGGCTCAAGCGGCGCAATCCCATCTGTGATTG 327
 QY 319 TGAGCTTGATCACTTCGCTATTGATCTCTCGGTAATTCATTGTTGGGAGGTACC 378
 DB 328 TCAGCTTCAACCTACGCTATTGATCTTTGAGTAATGATGTTGGCGAGGTACC 387
 QY 379 AAAAAGTTTGCAGATACGCTCAAGAGCTCAACCACTGACGCCAGTCACTCGGTATGG 438
 DB 388 CAAGATCTGCAGGTACAGCTCAAGGCTCACCCTGCGCGTC-----GTTCCGG 438
 QY 439 TTCCATTAATCATGCTATTGATGTGA---GCAGTAGAAGAACGCTCGATCAAGACCA 495
 DB 439 TTTCAACAATGCCATTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 498
 QY 496 TACAAATACAGGACCAACAATAGTGTGATCAGGAGCAACAATGTTTCCGGAA 555
 DB 499 TACAATATCTGGGACCAACAATCTGTGATCCGGGAGCAAAAATGTTGTTGCTGGAA 558
 QY 556 TGACAAACAGGCTCGTATCTGGGAATAACAACCATGTGCTGGAGCAACAACCTGTT 615
 DB 559 TGACAAACAGGCTCATATCTGGGACCAACAATAGTGTGCTGGAGCAACAACCTGCT 618
 QY 616 AACTGGAAGTGAACAATCTGTTAGTGTGATGCAACCATGCTGATCAGGACCAAGCATAT 675
 DB 619 AAGTGGGAGTGAACAATACCGTAACTGCGCAGCAACCATGCTGATCAGGACCAACATAT 678
 QY 676 TGTACTGATACAATAATGTTGATCCGGGACGACAATAATGCTCTGGAGCTTCCA 735

DB 679 CGTTACAGACAAACAATAACGTTATCCGGGAACGATAAATATGTTATCCGGAGCTTTCA 738
 QY 736 TACTGTATCAGGGAGGACAAATACGTTATCCGGAGCAACAATACTGTATCCGGAGCAA 795
 DB 739 TACCGTATCCGGGGGCAATACCGTCTCTGGGAGCAACAATACCGTATCTGGAGCA 798
 QY 796 CCATATCGTATCTGGGAGCAACAAGTCTGAACAGATGGTTAATATCTGTAGGTGCGAG 855
 DB 799 CCATGTTGTAATCTGGAAGCAACAAGTCTGACAGACGCTTAATGATCTGTGAGCGCATG 858
 QY 856 ATTGCTTCCATCTT-----CCCAAGTTTCAGTGTAGCTTACAATCAA 896
 DB 859 ATTTGTTCCACCTTAACTGAGCTCAGCTTCTTGTCCAAAGTTCACTGTACCTCACAGTCAG 918
 QY 897 TAGATGGAGACAATCACGTTATGTAACCTTCA-GGATATGGCATACTTTTC---CTTTAAA 952
 DB 919 TTGGTGCCTTCAATCGGCTTATGTAACCTTCATGATATACCATACTTTTCTCTACTATA 978
 QY 953 TAAAGCTTCCCTTTTACATAAAAAA 980
 DB 979 TAAATTTTCCCTTTAAAAA 1006

RESULT 4

ADMA1467
 ID ADMA1467 standard; cDNA; 1008 BP.
 XX AC ADMA1467;
 XX DT 03-JUN-2004 (first entry)
 XX DE Perennial ryegrass antifreeze protein APP5 cDNA.
 XX KW Antifreeze; perennial ryegrass; cold tolerance; transgenic; plant;
 XX OS Lolium perenne.
 XX FT CDS Location/Qualifiers
 FT sig_peptide /tag= b
 FT /product= "Antifreeze protein APP5"
 FT /tag= a
 FT mat_peptide /tag= c
 XX WO2004022700-A2.
 XX 18-MAR-2004.
 XX PF 09-SEP-2003; 2003WO-NZ000199.
 XX PR 09-SEP-2002; 2002US-0409557P.
 XX (GENE-) GENESIS RES & DEV CORP LTD.
 XX (WRIG-) WRIGHTSON SEEDS LTD.
 XX Demmer J, Shenk MA, Hall C, Fish SA;
 XX WPI: 2004-248453/23.
 XX P-PSDB; ADMA1480.
 XX New antifreeze proteins and encoding polynucleotides, useful for
 XX modulating cold tolerance in organisms, as food additives, or for
 XX treating tumors or disorders associated with the presence of unwanted
 XX biocrystals (e.g. gout).
 XX Claim 1; SEQ ID NO 10; 71pp; English.
 XX The present sequence is that of cDNA encoding APP5, an antifreeze protein
 XX of perennial ryegrass. The cDNA was isolated from a leaf blade cDNA
 XX expression library. The invention provides forage grass (perennial

Claim 1; SEQ ID NO 4; 71pp; English.

The present sequence is that of cDNA encoding an antifreeze protein of tall fescue. The cDNA was isolated from a leaf blade cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polynucleotides encoding them ADW41458-ADW41483. The polynucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polynucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze polypeptide. The antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive or a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to frost or freezing.

XX SQ Sequence 996 BP; 268 A; 235 C; 250 G; 243 T; 0 U; 0 Other;

Query Match 92.3%; Score 904.4; DB 12; Length 996;
Best Local Similarity 96.2%; Pred. No. 5,2e-273;
Matches 949; Conservative 0; Mismatches 31; Indels 6; Gaps 2

Qy 1 GCTTGCATTCCAATCAAGGTTTCCTTGTTCAATCCATGCTGAATACATGGCAAAGTGTTG 60
Db 7 GCTTGCATTCCAATCAAGGTTTCCTTGTTCAATCCATGCTGAATACATGGCAAAGTGTTG 66

Qy 61 CATGCTCGTGTCTCTCTGGGGTTCA --- TCTTCAGGTGGCAGCAGCAACTGCTGTGTC 117
Db 67 CATGCTCGTGTCTCTCTGGGGTTCAATCCTCTTCAGGTGGCGGAGCAACGTCGTGTGTC 126

Qy 118 GTGCCACCACGACGACCTCCACGGGCTTCAGGGGCTCGTGAGAACCCTAAGCGGCAAAAGG 177
Db 127 GTGCCACCACGACGACCTCCGGGCATTGAGGGGCTTCGGCAGAACCTTAAGCGGCAAAAGG 186

Qy 178 AGCGTCCGCTCCGCGCCGATGGTCGCGGCGCTCATGCTGCAGCTGGGAAGGTGTGGG 237
Db 187 AGCGTCCGCTCCGCGCCGATGGTCGCGGCGCTCATGCTGCAGCTGGGAAGGTGTGGG 246

Qy 238 ATGCGAAACAGACGCGCGCGTGTGGCGTTCGGGCTCCCCAAGCGCGGCTTGGAGG 297
Db 247 ATGCGAAACAGACGCGCGCGTGTGGCGTTCGGGCTCCCCAAGCGCGGCTTGGAGG 306

Qy 298 GATCATCCCATGTCGATTGGTAGCTTGATCACCTTCGCTATTGGAATCTCTCGGGTAA 357
Db 307 GACCATCCATCGTCGATTGGTAGCTTGATCACCTTCGTTGTTTGGATCTCTCGGGTAA 366

Qy 358 TTCAATGGTTGGGAGGTACCAAAAAGTTTCAGATA CGGCTCAAGAGCCTCACCACCTGA 417
Db 367 TTCATTGGTTGGGAAGGTACCAAAAAGTTTCAGATA CGGCTCTAGAGCCTCTCCACTGA 426

Qy 418 CAGCCAGTCACTCGGTATGGGTTCCATTAA CANGCTATTGCATGTGAGAGGT---AGAG 474
Db 427 TGGCCAGTCACTCGGTATGGGTTCCATTAA CACGCTATTGCATGTGAGCAGTAA CAGAAG 486

Qy 475 AACGCTCGATGAAGAACCAATACAATATCAGGGACCAACAATAGTGTGGATCAGGGAG 534
Db 487 AACCTCGATGAAGAACCAATACAATATCAGGGACCAACAATAGTGTGGATCAGGGAG 546

Qy 535 CAACAATGTTGTTTTCCGGGAATGCAACA CCGGTGCTATCTCGGGAATAACAACCATGTGTC 594
Db 547 CAACAATGTTGTTTTCCGGGAATGCAACA CCGGTGCTATCTCGGGAATAACAACCATGTGTC 606

Qy 595 TGGAGCAACAACACTGTTGTTAACTGGGAAGTGACAAT ACTGTAGTTGGTAGCAACCATGT 654
Db 607 TGGAGCAACAACACTGTTGTTAACTGGGAAGTGACAACACTTTAGTTGGTAGCAACCATGT 666

PT	biocrystals (e.g. gout).	
XX	Claim 1; SEQ ID NO 3; 71pp; English.	
PS	The present sequence is that of cDNA encoding APP2, an antifreeze protein	
CC	of perennial ryegrass. The cDNA was isolated from a leaf blade cDNA	
CC	expression library. The invention provides forage grass (perennial	
CC	ryegrass and tall fescue) antifreeze proteins and the polynucleotides	
CC	encoding them ADM41458-ADM41483. The polynucleotides were isolated from	
CC	tissues taken at different times of year (winter and spring) and from	
CC	different parts of the plants. The polynucleotides can be used to	
CC	modulate the cold tolerance of an organism, especially plants, mammals,	
CC	insects, fungi, archaea and bacteria. The method involves incorporating	
CC	an antifreeze polynucleotide, under the control of a gene promoter	
CC	sequence, into the genome of the organism, or introducing double-stranded	
CC	RNA corresponding to the polynucleotide into the cells of the organism,	
CC	thereby inhibiting expression of an antifreeze polypeptide. The	
CC	antifreeze protein can be used for the cryopreservation of a cell or	
CC	tissue, as a food additive of a frozen food product, in a method for	
CC	decreasing the time required to dehydrate a composition, to treat a	
CC	disorder characterised by biocrystals associated with disorders such as	
CC	gout and kidney stones, to preserve the viability of a molecular biology	
CC	reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and	
CC	to protect a plant from damage due to frost or freezing.	
XX		
SQ	Sequence 980 BP; 264 A; 223 C; 253 G; 240 T; 0 U; 0 Other;	
	Query Match 100.0%; Score 980; DB 12; Length 980;	
	Best Local Similarity 100.0%; Pred. No. 9e-297;	
	Matches 980; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 GCTTGCAATCCAAATCAAGGTTCTTGTTCAATCCATGCTCTGAATACATCGGCAAGTGTTG 60	
DB	1 GCTTGCAATCCAAATCAAGGTTCTTGTTCAATCCATGCTCTGAATACATCGGCAAGTGTTG 60	
QY	61 CATGCTGCTGGTCTTCTGGGTTTCATCTTGAGGTTGGCAGGCAACGTCGTGGTCTGG 120	
DB	61 CATGCTGCTGGTCTTCTGGGTTTCATCTTGAGGTTGGCAGGCAACGTCGTGGTCTGG 120	
QY	121 CCACACGACGACCTCCAGCGTTGAGGGGCTCGCTGAGAACCTTAAGCGCAAGGAGC 180	
DB	121 CCACACGACGACCTCCAGCGTTGAGGGGCTCGCTGAGAACCTTAAGCGCAAGGAGC 180	
QY	181 CGTCCGCTCCGCGCCGCAATGTCGCGGCTCATGCTGAGCTGGGAAGGTGTGGATG 240	
DB	181 CGTCCGCTCCGCGCCGCAATGTCGCGGCTCATGCTGAGCTGGGAAGGTGTGGATG 240	
QY	241 CGAAACGACGACGCGCGGTCGTGGCGTTGGGCTCCCAAGCGCGGCTTGGAGGGAT 300	
DB	241 CGAAACGACGACGCGCGGTCGTGGCGTTGGGCTCCCAAGCGCGGCTTGGAGGGAT 300	
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QY	661 AGGGACAAAGCATATTTTACTGATAACAATAATGTTGTTATCCGGGACGACAAATAATGT 720	
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QY	841 TTCTGTAGTGCAGGATTTGCTTCCATCTTCCCAAGTTCAGTGTAGCTTACATCAATAGA 900	
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Db	901 TGGGACAAATCACGTTATGTAACCTTCCAGATATGGCATACTTTCTTTAAATAAAGCTT 960	
QY	961 CCCTTTACATAAAAAAAA 980	
Db	961 CCCTTTACATAAAAAAAA 980	
RESULT 2		
ADM41461		
ID	ADM41461 standard; cDNA; 996 BP.	
XX	AC ADM41461;	
XX	DT 03-JUN-2004 (first entry)	
XX	Tall fescue antifreeze protein cDNA.	
DE	Antifreeze; fescue; cold tolerance; transgenic; plant; antigout;	
KW	litholytic; nephrotropic; cytostatic; gene; ss.	
XX	Schedonorus arundinaceus.	
OS	Key	
EH	Location/Qualifiers	
FT	CDS	
FT	41..850	
FT	/tag= b	
FT	/product= "Antifreeze protein"	
FT	/transl_except= (pos:410..412,aa:Xaa)	
FT	/note= "Xaa= unknown"	
FT	sig_peptide	
FT	41..112	
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XX	WO2004022700-A2.	
PN	18-MAR-2004.	
PD	09-SEP-2003; 2003WO-NZ0000199.	
XX	09-SEP-2002; 2002US-0409557P.	
XX	(GENE-) GENESIS RES & DEV CORP LTD.	
PA	(WRIG-) WRIGHTSON SEEDS LTD.	
XX	Demmer J, Shenk MA, Hall C, Fish SA;	
PI	WPI: 2004-248453/23.	
XX	P-PSDB; ADM41474.	
DR	New antifreeze proteins and encoding polynucleotides, useful for	
PT	modulating cold tolerance in organisms, as food additives, or for	
PT	treating tumors or disorders associated with the presence of unwanted	
PT	biocrystals (e.g. gout).	

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OM nucleic - nucleic search, using sw model

Run on: October 8, 2005, 10:18:05 ; Search time 572 Seconds
(without alignments)
10142.214 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
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2	904.4	92.3	996 12 ADM41461 Tall fesc
3	541.6	55.3	1006 12 ADM41468 Tall fesc
4	503.6	51.4	1008 12 ADM41467 Perennial
5	492.8	50.3	1007 12 ADM41469 Perennial
6	451.2	46.0	1230 12 ADM41463 Tall fesc
7	443.6	45.3	1212 12 ADM41464 Perennial
8	421.8	43.0	1246 12 ADM41466 Tall fesc
9	419	42.8	1083 12 ADM41470 Perennial
10	417.4	42.6	1084 12 ADM41462 Perennial
11	394.4	40.2	1064 12 ADM41465 Perennial
12	270.4	27.6	959 12 ADM41459 Tall fesc
13	264.2	27.0	357 2 AAX99717 Grass ant
14	262.2	26.8	841 12 ADM41458 Perennial
15	79.4	8.1	4536 12 ADJ40496 Plant cDN
16	54	5.5	2000 8 ADA71938 Rice gene
17	51.8	5.3	1138 1 AAN91630 3' sequen
18	50.6	5.2	1912 12 ADJ39568 Plant cDN
19	48.2	4.9	3000 12 ADI32615 Rice tran
20	44.8	4.6	3453 3 AAA97909 Eucalyptu

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C	22	43	4.4	7722	3	AAA70168	Aaa70168 Plasmodiu
C	23	41.6	4.2	2274	4	ABL17081	Abli17081 Drosophil
C	24	41.6	4.2	4274	4	ABL17080	Abli17080 Drosophil
C	25	41.4	4.2	966	6	ABQ17272	Abqi17272 Oligonuc
C	26	41.4	4.2	966	6	ABQ17273	Abqi17273 Oligonuc
C	27	41	4.2	408	3	AAA79411	Aaa79411 Eucalyptu
C	28	40.8	4.2	702	5	AA567541	Aas67541 DNA encod
C	29	40.4	4.1	396	3	AAA79420	Aaa79420 Eucalyptu
C	30	40.4	4.1	3381	2	AAV41343	Aav41343 M. catarr
C	31	40.4	4.1	12614	4	AAI99322	Aai99322 Human exc
C	32	40.4	4.1	12614	4	AAI63672	Aai63672 Human kid
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C	34	40	4.1	804	12	ADM80069	Adm80069 Spiramyci
C	35	40	4.1	804	12	ADN97585	Adn97585 S ambofac
C	36	40	4.1	30943	12	ADM80034	Adm80034 Spiramyci
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C	41	39.6	4.0	4298	4	ABL18480	Abli18480 Drosophil
C	42	39.2	4.0	1443	10	ABZ23668	Abz23668 H. pylori
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C	45	38.8	4.0	1028	3	AAA50251	Aaa50251 Maize hea

ALIGNMENTS

RESULT 1

ADM41460

ID ADM41460 standard; cDNA; 980 BP.

XX ADM41460;

DT 03-JUN-2004 (first entry)

XX Perennial ryegrass antifreeze protein AFP2 cDNA.

KW Antifreeze; perennial ryegrass; cold tolerance; transgenic; plant;

KW antitgout; litholytic; nephrotropic; cytotstatic; gene; ss.

XX Lolium perenne.

XX Key Location/Qualifiers

FT CDS 35..838

FT /*tag= b

FT /product= "Antifreeze protein AFP2"

FT sig_peptide 35..103

FT /*tag= a

FT mat_peptide 104..835

FT /*tag= c

FT WO2004022700-A2.

XX 18-MAR-2004.

XX 09-SEP-2003; 2003WO-NZ000199.

XX 09-SEP-2002; 2002US-0409557P.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX P-PSDB; ADM41473.

XX Demmer J, Shenk MA, Hall C, Fish SA;

XX WPI; 2004-248453/23.

XX P-PSDB; ADM41473.

XX New antifreeze proteins and encoding polynucleotides, useful for

XX modulating cold tolerance in organisms, as food additives, or for

XX treating tumors or disorders associated with the presence of unwanted

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Db 172320 AGCATGTATCAGCACTGGGGTAGCATGTATCAGCACTGTTGTAGCATGTATCAGCACTTT 172261
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Search completed: October 8, 2005, 19:05:38
Job time : 4305 secs

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TITLE
JOURNAL
REFERENCE
AUTHORS

Direct Submission
Unpublished
2 (bases 1 to 261587)
Worley, K.C.

TITLE
JOURNAL

Submitted (04-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 261587)
Rat Genome Sequencing Consortium.

REFERENCE
AUTHORS
TITLE
JOURNAL

Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:24819414.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

COMMENT

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GHUJ
Center clone name: CH230-104014
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 245312 bases at least Q40
Consensus quality: 249138 bases at least Q30
Consensus quality: 252151 bases at least Q20
Estimated insert size: 257796; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
* NOTE: This sequence may represent more than one clone.
* NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
* 1 250010: contig of 250010 bp in length
* 250011 250110: gap of unknown length
* 250111 253467: contig of 3357 bp in length
* 253468 253567: gap of unknown length

* 253568 255148: contig of 1581 bp in length
* 255149 255248: gap of unknown length
* 255249 256807: contig of 1559 bp in length
* 256808 256907: gap of unknown length
* 256908 258585: contig of 1678 bp in length
* 258586 258685: gap of unknown length
* 258686 260166: contig of 1481 bp in length
* 260167 260266: gap of unknown length
* 260267 261587: contig of 1321 bp in length.

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Matches 165; Conservative 0; Mismatches 147; Indels 6; Gaps 1;
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Db 83753 ATCAGCACTGTTGTAGCATGTATCAGCACTGTTGTAGCATGTATCAGCACTTTTGTAGCA 83694
QY 572 TCTGGGAATAACAACCATGTGCTCGGAGCAACAACACATGTTGTAACATGCAAT 631
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QY 632 ACTGTAGTTGGTAGCAACCATGTCGTATCAGGAGCAAAAGCATATTGTTACTGATAACAAT 691
Db 83639 GTTGTAGCATGTATCAGCACTGTTGTAGCATGTATCAGCACTGTGTTAATGATATCAGC 83580
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RESULT 15

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DEFINITION Rattus norvegicus clone CH230-462N7, WORKING DRAFT SEQUENCE.
ACCESSION AC119701
VERSION AC119701.7 GI:25137804
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

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DB 233763 TTGTTCAAGGTTATTACAATATGTTTCAAGGTTATTACAATATGTTTCAAGGTTATTACA 233822

QY 840 ATTCTGT 846
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RESULT 13
CQ741677
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Q741677
Sequence 27611 from Patent WO02068579.
CQ741677
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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
Patent: WO 02068579-A 27611 06-SEP-2002;
PE Corporation (NY) (US)
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AC126139 261587 bp DNA linear HTG 10-MAY-2003
Rattus norvegicus clone CH230-104014, WORKING DRAFT SEQUENCE, 7
unordered pieces.
AC126139
AC126139.7 GI:30520607
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
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Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A.,
Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorensheva, L., Louiseged, H., Lozano, R. J., Lu, X., Ma, J.,
Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mawhiney, S., McLeod, M. P., McNeill, T. Z., Meenen, E.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
Nankervis, C., Neal, D., Newcon, N., Nguyen, N., Norris, S., Parks, K.,
Nwaokelemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C.,
Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L. L.,

TITLE Direct Submission
JOURNAL Submitted (24-FEB-1999) P.falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 1SA, UK
COMMENT On Oct 3, 2002 this sequence version replaced gi:5731897.
For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/projects/p_falciparum.
FEATURES Location/Qualifiers

source 1..347582
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Similar to Plasmodium falciparum rifin pfb0030C
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3.4e-65, 53.6% id in 375 aa"
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fasta scores: E(): 6.2e-103, 43.31% id in 3551 aa"
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10 - 19 : 48
 20 - 29 : 165
 30 - 39 : 825
 40 - 49 : 3919
 50 - 59 : 6201
 60 - 69 : 8574
 70 - 79 : 22106
 80 - 89 : 54448
 90 - 99 : 79950

Percentage of bases with a quality value >= 40 : 99 %.

FEATURES

source

Location/Qualifiers

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/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="14"

/clone_lib="RPCL-11"

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RHdb:RH7974

dbSTS:STS21065

Identified using the e-PCR software (G. Schuler)"

/note="matching EMBL:L00022"

RHdb:RH68981

dbSTS:STS48887

Identified using the e-PCR software (G. Schuler)"

60040..60260

/note="matching EMBL:M55420"

RHdb:RH80278

dbSTS:STS56700

Identified using the e-PCR software (G. Schuler)"

69316..69421

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RHdb:RH44850

dbSTS:STS37918

Identified using the e-PCR software (G. Schuler)"

145938..146060

/note="matching EMBL:253040"

RHdb:RH9751

dbSTS:STS5550

Identified using the e-PCR software (G. Schuler)"

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/note="matching EMBL:AA160692"

RHdb:RH49485

dbSTS:STS41544

Identified using the e-PCR software (G. Schuler)"

ORIGIN

Query Match 7.2%; Score 70.2; DB 9; Length 176237;

Best Local Similarity 56.5%; Pred. No. 2.8e-07;

Matches 130; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 600 GCAACAACTGTTGTAACCTGGAAGTGAACAATACTAGTGTAGCAACCAATGTCGTAT 659

Db 7784 GAAGCATCCAGATGGAACAGGAAATGTCCAGCATGGAACAGGAGCATCCAGAAATGTA 7725

QY 660 CAGGGCAAGCATATTTACTGTAAACAATAATTTGTATCCGGAGACGACAATAATG 719

Db 7724 CAGGAAGCATCCAGATGGAACAGGAAATGTCCAGCATGGAACAGGAGCATCAAGAAATG 7665

QY 720 TGTCTGGAAGCTTCCATCTGTATCAGGGAGGACAAATACCGTATCCGGAGCAACAATA 779

Db 7664 TAACAGAGCATCCAGATGGAACAGGAAATGTCCAGCATGGAACAGGAGCATCCAGA 7605

QY 780 CTGTATCCGGAGCAACCATATCGTATCTGGGAGCAACAAGTCGTAACA 829

Db 7604 ATGTACAGAGCATCCAGCATGGAACAGGAAATGTCCAGTGGAAACA 7555

RESULT 10

CNS01DT2

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CNS01DT2 169802 bp DNA linear PRI 19-NOV-2001
 Human chromosome 14 DNA sequence BAC R-417P24 of library RPCL-11
 from chromosome 14 of Homo sapiens (Human), complete sequence.

AL122127 GI:17026193

HTG.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 169802)

Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,

Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F.,

Levy,M., Eckenberg,R., Bruls,T., Desferdini,V., Cruaud,C.,

Gyapay,G., Saurin,W. and Weissbach,J.

Sequencing of the human chromosome 14

Unpublished

2 (bases 1 to 169802)

Genoscope.

Direct Submission

Submitted (19-NOV-2001) Genoscope - Centre National de Sequencage :

Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

On Nov 20, 2001 this sequence version replaced gi:14715169.

----- Genome Center

Center: Genoscope / Centre National de Sequencage

Center code: GS

Web site: http://www.genoscope.cns.fr/

Contact: SeqRef@genoscope.cns.fr

The following BAC sequence is oriented from the T7 to the SP6 end.

----- Summary Statistics

Assembly program: Phrap; version 2.0

Quality coverage: 7.56x in Q20 bases; sum-of-contigs

Overall quality chart :

Range : bases

0 : 9

10 - 19 : 11

20 - 29 : 159

30 - 39 : 4325

40 - 49 : 11964

50 - 59 : 13264

60 - 69 : 28113

70 - 79 : 55713

80 - 89 : 56253

90 - 99 : 56253

Percentage of bases with a quality value >= 40 : 99 %.

----- Location/Qualifiers

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/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="14"

/clone_lib="RPCL-11"

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RHdb:RH67749

dbSTS:STS47676

Identified using the e-PCR software (G. Schuler)"

11439..11536

/note="matching EMBL:G14654"

RHdb:RH7974

dbSTS:STS21065

Identified using the e-PCR software (G. Schuler)"

39191..39405

/note="matching EMBL:G33053"

RHdb:RH67749

FEATURES

source

STS

STS

STS

SOURCE	Oryza sativa (japonica cultivar-group)	/translation="MTAGRCFAGARRHGRQARAGAAAGDGGDQDAVHHGHTRRADATGG
ORGANISM	Oryza sativa (japonica cultivar-group)	AAAAGQDRVTTARTARHGQPRGRANDARGAAARERGGELGSAPALAAHARGQS
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	GAERAREKESERREGGDPREIRPIDPGGKIDFCGGI"
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	complement(1507. .1932)
	Ehrhartoideae; Oryzeae; Oryza.	/gene="P0585H11.102"
REFERENCE	1	complement(<1507. .>1932)
AUTHORS	Sasaki,T., Matsumoto,T. and Yamamoto,K.	/gene="P0585H11.102"
TITLE	Oryza sativa nipponbare (G3) genomic DNA, chromosome 7, PAC	/note="start and end point are not identified"
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JOURNAL	Published Only in Database (2001)	/gene="P0585H11.102"
REFERENCE	2 (bases 1 to 149371)	/note="predicted by GlimmerM etc."
AUTHORS	Sasaki,T., Matsumoto,T. and Yamamoto,K.	/codon_start=1
TITLE	Direct Submission	/product="hypothetical protein"
JOURNAL	Submitted (14-NOV-2001) Takuji Sasaki, National Institute of	/protein_id="BAC20735.1"
	Agrbiological Sciences, Rice Genome Research Program; Kamondai	/db_xref="GI:23617047"
	2-1-2, Tsukuba, Ibaraki 305-8602, Japan	/translation="MRRHAQPHGRWNAWTCCTDRGPDPIAELVPTWRLGAYVA
	(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,	ATRAGGRKTASAANRAAAVSPGRLATMRGDGAYTQWTKRERANGLDSPGAR
	Tel:81-298-38-7441, Fax:81-298-38-7468)	QRISAATGGEQRGRHGGPIGGESIYAATGIRC"
COMMENT	On Jul 22, 2004 this sequence version replaced gi:34395173.	complement(5704. .6661)
	Genes were predicted from the integrated results of the following:	/gene="P0585H11.104"
	GENSCAN (http://ccr-081.mit.edu/GENSCAN.html), FGENESH	complement(5704. .6661)
	(http://www.softberry.com/), GeneMark.hmm	/gene="P0585H11.104"
	(http://opal.biology.gatech.edu/GeneMark/), GlimmerM	/note="supported by full-length cDNA(s): AK106062"
	(http://www.tigr.org/tdb/glimmer/glmr form.html), RiceHMM	5872. .6872
	(http://www.affrc.go.jp/RiceHMM/), SplicePredictor	/gene="P0585H11.103"
	(http://bioinformatics.fasstate.edu/cgi-bin/sp.cgi), sim4	<5872. .>6872
	(http://globin.cse.psu.edu/html/docs/sim4.html), gap2	/gene="P0585H11.103"
	(http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The	/note="supported by full-length cDNA(s): AK109288"
	genomic sequence was searched against NCBI Nonredundant Protein	5872. .6872
	database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA	/gene="P0585H11.103"
	sequence database at RGP or DDBJ. Protein homologies of the coding	/note="contains full-length cDNA(s): AK109288
	regions were searched against NCBI Nonredundant Protein database	non-coding transcript
	with BLASTP. ESTs represent the identified cDNA sequences using	probably inactive due to including stop codon(s) in CDS"
	BLASTN with the corresponding DDBJ accession no. and RGP clone ID.	complement(5942. .6631)
	Full-length cDNAs represent the identified cDNA sequences using	/gene="P0585H11.104"
	BLASTN with the corresponding DDBJ accession no.	/note="contains EST(s): AU101213 (E2609), C72987 (E2609)
	A gene with identity or significant homology to a protein is	contains full-length cDNA(s): AK106062"
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	such as same name, 'putative-' and '-like protein'. A gene without	/product="putative disease resistance response
	significant homology to any protein but with full-length cDNA or	protein-related/dirigent protein-related"
	EST homology (covering almost the entire length of partial	/protein_id="BAC20736.1"
	sequence) is classified as an 'unknown' protein. A gene predicted	/db_xref="GI:23617048"
	by two or more gene prediction programs is classified as a	/translation="MAPTSRSPAALFLLLALACAAAPLLRAADTHLHFFMHVWSGG
	'hypothetical' protein according to IKGSP standard. A gene	QTAQVVIKPTSAAGVTSQDVTVDALTTETSSATSPVGAQGYMMSLSSPT
	predicted by a single gene prediction program is also classified as	LMMCNLFTAGENNSTIAVGHDDTTATVRELSVGGTGKFMATGYVVKTSMS
	a probable 'hypothetical' protein and is included as a	ASTGVFEDVYVTTNATTIDASAPVPLDGGSGSGSTAKSGAAGRQGVWVSACV
	miscellaneous feature of the sequence.	GLVVALVGRGW"
	The orientation of the sequence is from T7 to SP6 of the PAC clone.	complement(8221. .8754)
	This sequence of P0585H11 clone has an overlap with B1317D11 (DDBJ:	/gene="P0585H11.105"
	AP006186) clone at 5' end and with OJ1567 (DDBJ: AP003759) at 3'	complement(join(<8221. .8529,8623. .>8754))
	end. Detailed information on overlap and assembly quality together	/note="start and end point are not identified"
	with annotation of this entry is available at	complement(join(8221. .8529,8623. .8754))
	http://rgp.dna.affrc.go.jp/GenomeSeq.html.	/gene="P0585H11.105"
FEATURES	Location/Qualifiers	/note="predicted by GeneMark.hmm etc."
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	/cultivar="Nipponbare"	/db_xref="GI:34395174"
	/db_xref="taxon:39947"	/translation="MAVTGVGVLDGGWRWQCASTRWNISGGDGLLLWSRWVVE
	/chromosome="7"	ATAGCTPWSDRWCLSRVNSLENISLRSPVAHRRFNSITAAAEERAPILGSL
	/clone="P0585H11"	WNGVCTGHDLVVSSCMPLPQSSSSSQDQLICSHNAPMLKVG"
	complement(298. .792)	complement(14091. .14753)
gene	/gene="P0585H11.101"	/gene="P0585H11.106"
mRNA	complement(join(<298. .591,655. .>792))	complement(<14091. .>14753)
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	/note="start and end point are not identified"	/note="start and end point are not identified"
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	/notes="similar to Oryza sativa chromosome 1, P0409B08.8"	/codon_start=1
CDS	/codon_start=1	/product="putative disease resistance response
	/product="hypothetical protein"	protein-related/dirigent protein-related"
	/protein_id="BAC20734.1"	/protein_id="BAC20739.1"
	/db_xref="GI:23617046"	

QY 782 GTATCGGGAGCAACCATATCGTATCTGGGAGCAACAAGTCTGAACAGATGTTAA 838
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Db 301 GTATCTGGGAGCAACCATGTTGTATCTGGGAGCAACAAGTCTGGAGACGCTTAA 357
|||||

AK121984 3392 bp mRNA linear PLN 29-OCT-2003
Oryza sativa (japonica cultivar-group) cDNA clone:J033108010, full
insert sequence.
AK121984
AK121984.1 GI:37991607
FLI CDNA; CAP trapper
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS
The Rice Full-length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-length cDNA Project Team:
Kikuchi S., Satoh K., Nagata T., Kawagashira N., Doi K.,
Kishimoto N., Yazaki J., Ishikawa M., Yamada H., Ooka H., Hotta I.,
Kojima K., Namiki T., Ohneda E., Yahagi W., Suzuki K., Li C.,
Ohtsuki K., Shishiki T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group: Ohtomo Y., Murakami K.,
Iida Y., Sugano S., Fujimura T., Suzuki Y., Tsunoda Y.,
Kurosaki T., Kodama T., Masuda H., Kobayashi M., Xie Q., Lu M.,
Narikawa R., Sugiyama A., Mizuno K., Yokomizo S., Niikura J.,
Ikeda R., Ishibiki J., Kawamata M., Yoshimura A., Miura J.,
Kusumegi T., Oka M., Ryu R., Ueda M., Matsubara K., RIKEN,
Kawai J., Carninci P., Adachi J., Aizawa K., Arakawa T., Fukuda S.,
Hara A., Hashidume W., Hayatsu N., Imotani K., Ishii Y., Itoh M.,
Kagawa I., Kondo S., Konno H., Miyazaki A., Osato N., Ota Y.,
Saito R., Sasaki D., Sato K., Shibata K., Shinagawa A., Shiraki T.,
Yoshino M. and Hayashizaki Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
Science 301 (5631), 376-379 (2003)
JOURNAL
MEDLINE
22752273
12869764
PUBMED
2
REFERENCE
AUTHORS

Adachi J., Aizawa K., Akimura T., Arakawa T., Carninci P., Doi K.,
Fujimura T., Fukuda S., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayashizaki Y., Hayatsu N., Hiramoto K., Hiraoka T.,
Hori F., Hotta I., Iida J., Iida Y., Ikeda R., Imamura K.,
Imotani K., Ishibiki J., Ishii Y., Ishikawa M., Itoh M., Kagawa I.,
Kanagawa S., Katoh H., Kawagashira N., Kawai J., Kawamata M.,
Kikuchi S., Kishikawa-Hirozane T., Kishimoto N., Kobayashi M.,
Kodama T., Kojima K., Kojima Y., Kondo S., Konno H., Kouda M.,
Koya S., Kurihara C., Kurosaki T., Kusumegi T., Li C., Lu M.,
Masuda H., Matsubara K., Matsuyama T., Miura J., Miyazaki A.,
Mizuno K., Murakami K., Murata M., Nagata T., Nakahama Y.,
Nakamura M., Namiki T., Narikawa R., Niikura J., Nishi K.,
Nomura K., Numasaki R., Ohneda E., Ohno M., Ohtsuki K., Oka M.,
Ooka H., Osato N., Ota Y., Ohtomo Y., Ryu R., Saitoh H., Sakai C.,
Sakai K., Sakazume N., Sano H., Sasaki D., Sato K., Satoh K.,
Shibata K., Shinagawa A., Shiraki T., Shishiki T., Sogabe Y.,
Sugano S., Sugiyama A., Suzuki K., Suzuki Y., Tagami M.,
Tagami-Takeda Y., Tagawa A., Takahashi F., Takaku-Akahira S.,
Tanaka T., Tomaru A., Toya T., Tsunoda Y., Ueda M., Waki K.,
Xie Q., Yahagi W., Yamada H., Yamamoto M., Yasunishi A., Yazaki J.,
Yokomizo S. and Yoshimura A.

Collection, mapping, and annotation of 28K full-length cDNA clones
from japonica rice
Unpublished
3 (bases 1 to 3392)
Kikuchi S.
Direct Submission
Submitted (31-JAN-2003) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki

305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 32K full-length cDNA clones from japonica
rice.

URL : http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-length cDNA Project Team: Kikuchi S., Satoh K.,
Nagata T., Kawagashira N., Doi K., Kishimoto N., Yazaki J.,
Ishikawa M., Yamada H., Ooka H., Hotta I., Kojima K., Namiki T.,
Ohneda E., Yahagi W., Suzuki K., Li C., Ohtsuki K., Shishiki T.,
Yamamoto M. and Nakahama Y.
FAIS Genome Sequencing & Analysis Group: Ohtomo Y., Iida Y.,
Fujimura T., Ikeda R., Ishibiki J., Kawamata M.,
Kobayashi M., Kodama T., Kurosaki T., Kusumegi T., Lu M.,
Masuda H., Miura J., Mizuno K., Narikawa R., Niikura J., Oka M.,
Ryu R., Sugano S., Sugiyama A., Suzuki Y., Tsunoda Y., Ueda M.,
Xie Q., Yokomizo S., Yoshimura A., Matsubara K. and Murakami K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi J., Aizawa K.,
Akimura T., Arakawa T., Carninci P., Fukuda S., Hanagaki T.,
Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K.,
Hirooka T., Hori F., Iida J., Imamura K., Imotani K., Ishii Y.,
Itoh M., Kagawa I., Kanagawa S., Katoh H., Kawai J.,
Kishikawa-Hirozane T., Kojima Y., Kondo S., Konno H., Kouda M.,
Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M.,
Nakamura M., Nishi K., Nomura K., Numasaki R., Ohno M., Osato N.,
Ota Y., Saitoh H., Sakai C., Sakai K.,
Sakazume N., Sano H., Sasaki D., Sato K., Shibata K.,
Shinagawa A., Shiraki T., Sogabe Y., Tagami F.,
Tagami-Takeda Y., Tagawa A., Takahashi F.,
Takaku-Akahira S., Tanaka T., Tomaru A., Toya T., Waki K.,
Yasunishi A. and Hayashizaki Y.

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Matches 157; Conservative 0; Mismatches 86; Indels 6; Gaps 2;
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Db 202 GCTGCGCGCGCCATGCCACCGGAAGACCTCTCTCGCGCTGCGGGGAAT 261
QY 164 CT--AAGCGGCAAGAGGAGCGCTCGCGCTCCGCGCGCATGGTCCGCGCCTCATGCTGC 220
Db 262 CTCTCTGCGGTTGGGGCGCGCGCGGACATCCGCGCGCGCTGTCGGGTACGCGCTGCTGC 321
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Db 322 GCCTGGGACGGCGTGCCTGCGCGACGCGCG--CGCCGAGTCAACGCGCTGCGCTCCCC 378
QY 281 AAGCGCGCGCTTGGAGAGGATCATCCCATCGTCGATGGTGGAGTTCACCTTCGCTAT 340
Db 379 GGCGCGAGGTCTCGAGGGGCCCATCCCGCGCTCCCTCGCGCGCTCGCGCGCTCCAGGAC 438
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RESULT 5
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LOCUS
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DEFINITION
PAC clone:F0585H11.
ACCESSION
AP004342
VERSION
AP004342.5 GI:50510014
KEYWORDS

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RESULT 2
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DEFINITION Sequence 2 from Patent WO9937782.
ACCESSION AX019971
VERSION AX019971.1 GI:10043803
KEYWORDS
SOURCE Loliium perenne
ORGANISM Loliium perenne
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Poae; Loliium.
REFERENCE 1
AUTHORS Twigg, S., Worrall, D., Jarman, C.D. and Sidebottom, C.M.
TITLE Frozen food product
JOURNAL Patent: WO 9937782-A 2 29-JUL-1999;
TWIGG SARAH (GB); UNILEVER PLC (GB); WORRALL DAWN (GB); JARMAN CARL
DUDLEY (GB); SIDEBOTTOM CHRISTOPHER MICHAEL (GB); UNILEVER NV (NL)
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Qy 542 GTTGTTCGGGAATGACAAACGCTGCTATCTGGGAATAACAACCATGTGTCTGGGAGC 601
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Qy 662 GGGCAAAAGCATATTTACTGATACCAATATTTGTTATCTCGGGAACGACCAATAATGTG 721
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DEFINITION Loliium perenne partial mRNA for ice recrystallisation inhibition protein.
ACCESSION AJ277399
VERSION AJ277399.1 GI:7573547
KEYWORDS ice recrystallisation inhibition protein.
SOURCE Loliium perenne
ORGANISM Loliium perenne
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Poae; Loliium.
REFERENCE 1
AUTHORS Sidebottom, C.M.
JOURNAL Thesis (1999) University of York
2. (bases 1 to 357)
REFERENCE Sidebottom, C.M.
AUTHORS
TITLE Direct Submission
JOURNAL Submitted (11-APR-2000) Sidebottom C.M., Plant Science, Unilever Research, Colworth House, Sharnbrook, Bedfordshire, MK44 1LQ, UNITED KINGDOM
COMMENT cds represents presumed mature peptide generated by cleavage before the first amino acid.
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Location/Qualifiers
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ORIGIN
Query Match 27.0%; Score 264.2; DB 8; Length 357;
Best Local Similarity 83.8%; Pred. No. 2.4e-60;
Matches 299; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
Qy 482 GATGAAGCAACCAATACCAATATCAGGACCAACAATAGTTGGATCAGGAGCAACAAT 541
Db 1 GATGAACCGCAATACGATTCTCGGAGCAACATATCTGCAGATCGGAGCAAAAT 60
Qy 542 GTTGTTCGGGAATGACAAACGCTGCTATCTGGGAATAACAACCATGTGTCTGGGAGC 601
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Qy 662 GGGCAAAAGCATATTTACTGATACCAATATTTGTTATCTCGGGAACGACCAATAATGTG 721
Db 181 GGGCAAAAGCATATTTACTGATACCAATATTTGTTATCTCGGGAACGACCAATAATGTG 240
Qy 722 TCTGGAAGTTCATCTGATCTAGGAGGACCAATACCGTATCCGGGAGCAACAATACT 781
Db 241 TCCGGAGCTTTCATACCGTATCCGGGGGACCAATACTGTCTCGGAGCAACAATACC 300

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2005, 10:25:15 ; Search time 4298 Seconds

(without alignments)
11048.421 Million cell updates/sec

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Searched: 4708233 seqs, 24227607955 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	79.4	8.1	3392	8	AK121984	AK121984 Oryza sat
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7	74.8	7.6	2238	8	AK064359	AK064359 Oryza sat
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12	63.8	6.5	347582	3	PFMAL4P1	AL034557 Plasmodiu
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15	59.6	6.1	172527	2	AC119701	AC119701 Rattus no
16	58.2	5.9	290724	2	AC098103	AC098103 Rattus no
17	57.8	5.9	231341	5	BX004816	BX004816 Zebrafish
18	55.8	5.7	243639	2	AC109943	AC109943 Rattus no
19	55.2	5.6	342650	1	AP003582	AP003582 Nostoc sp

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c 22	54.2	5.5	255300	2	AC128061	AC128061 Rattus no
c 23	54	5.5	2000	6	AX655393	AX655393 Sequence
c 24	54	5.5	167601	10	AC144408	AC144408 Mus muscu
c 25	54	5.5	217131	10	AC126053	AC126053 Mus muscu
c 26	53.6	5.5	56310	2	AC084717	AC084717 Homo sapi
c 27	53.6	5.5	222930	2	AC099698	AC099698 Mus muscu
c 28	53.6	5.5	289405	2	AC090126	AC090126 Mus muscu
c 29	53.2	5.4	110000	1	CR522870_00	CR522870 Desulfoka
c 30	53.2	5.4	158901	2	AC145786	AC145786 Xenopus t
c 31	52.6	5.4	41951	2	AC139177	AC139177 Clona sav
c 32	52.4	5.3	10029	1	AE010994	AE010994 Methanosa
c 33	52.2	5.3	109137	2	AC116969	AC116969 Rattus no
c 34	52.2	5.3	172750	2	AC119495	AC119495 Rattus no
c 35	52.2	5.3	217434	2	AC133239	AC133239 Rattus no
c 36	52.2	5.3	236346	2	AC095765	AC095765 Rattus no
c 37	52	5.3	5940	8	THA133651	THA133651 Trichoder
c 38	51.8	5.3	1138	6	E02599	E02599 DNA encodin
c 39	51.8	5.3	4215	9	HSS1GMG4	X12843 Human sigma
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LOCUS	BD139942	Freezed foods.			
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ACCESSION	BD139942.1	GI:23234887			
VERSION	JP 2002504316-A/1.				
KEYWORDS	Lolium perenne				
SOURCE	Lolium perenne				
ORGANISM	Lolium perenne				
REFERENCE	1 (bases 1 to 357)				
AUTHORS	Jarman,C.D., Sidebottom,C.M., Twigg,S. and Worrall,D.				
TITLE	Freezed foods				
JOURNAL	Patent: JP 2002504316-A 1 12-FEB-2002;				
COMMENT	UNILEVER NV				
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	PN JP 2002504316-A/1				
	PD 12-FEB-2002				
	PF 23-DEC-1998 JP 2000528689				
	PI 22-JAN-1998 GB 9801408.7				
	PI CARL DUDLEY JARMAN, CHRISTOPHER MICHAEL SIDEBOTTOM, SARAH TWIGG,				
	PI DAWN WORRALL				
	PC C12N15/09, A01H5/00, A23G9/02, A23L3/375, C07K14/415, C12N15/00 CC				
	Freezed foods				
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FEATURES	source				
ORIGIN					
Query Match	27.0%;	Score 264.2;	DB 6;	Length 357;	
Best Local Similarity	83.8%;	Pred. No. 2.4e-60;			
Matches 299;	Conservative 0;	Mismatches 58;	Indels 0;	Gaps 0;	
QY	482	GATGAAGAACCAATAATATCAGGACCAACAAATAGTGTGGATCAGGAGCAACAAT	541		